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(54) Title: NUCLEIC ACID SEQUENCES FROM DROSOPHILA MELANOGASTER THAT ENCODE PROTEINS ESSENTIAL FOR LARVAL VIABILITY AND USES THEREOF

(57) Abstract: Nucleotide sequences are isolated from Drosophila melanogaster that code for proteins essential for larval viability. These proteins are useful for discovering newinsecticides based on the essentiality of the nucleotide sequences for Drossophila larval viability. Further provided are recombinant proteins and methods for identifying inhibitors to these proteins. Protein inhibitors active in the methods disclosed herein are useful as insecticidal, ectoparasiticidal, antiparasitic, anthementhic and acaracidal agents.

NUCLEIC ACID SEQUENCES FROM *DROSOPHILA MELANOGASTER* THAT ENCODE PROTEINS ESSENTIAL FOR LARVAL VIABILITY AND USES THEREOF

This application claims the benefit of U.S. Provisional Application No. 60/262,351, filed January 18, 2001, incorporated herein by reference.

FIELD OF INVENTION

The present invention pertains to nucleic acid sequences isolated from *Drosophila melanogaster* that encode proteins essential for larval viability. The invention particularly relates to methods of using these proteins as insecticide targets, based on this essentiality.

BACKGROUND OF THE INVENTION

Insects contribute or cause many human and animal diseases, and are responsible for substantial agricultural and property damage. The societal costs associated with insect pests in dollars, time and suffering are monumental. The total worldwide market size for insecticide crop protection is over $5 billion. To combat these problems, insecticidal compounds have been developed and employed.

The idea to use chemicals for insect control is not new. The scientific use of pesticides started with the introduction of arsenical insecticides and organic compounds such as tar, petroleum oils, and dinitrophenol emulsions at the end of the last century. But, the systematic search for synthetic organic insecticides was only launched after the discovery of the insecticidal properties of DDT in 1939. After World War II, chemical research concentrated mainly on chlorinated hydrocarbons and cyclodienes, which all require high rates of application and have a rather broad spectrum of activity. Most of them are persistent in the environment and may pose a significant risk for accumulation in the food chain. Today the use of these chemicals is very much restricted.

From this point, the major emphasis in research has been given to organophosphates and carbamates, which are readily degradable in the environment with little tendency for bioaccumulation. The toxicity of these compounds varies within a broad range from medium to highly toxic. Organophosphates and carbamates are still widely use, although the more

toxic ones are banned in certain countries. The formamidines have as their major advantage a different mode of action and their selectivity, which made them suitable for use in IPM (insect pest management) programs. They are easily degradable with no accumulation potential, but for toxicological reasons some have had to be withdrawn from the market.

For the past decade, insecticide research has concentrated on leadfinding for new chemical structures interfering with new target mechanisms. The chances for success are rather remote, because the hurdles for the registration of a new insecticide are set very high. Toxicological aspects, insecticide resistance, environmental behavior, and IPM fitness are some of the critical factors that have to be considered together with economical factors.

Novel insecticides can now be discovered using high-throughput screens that implement recombinant DNA technology. Proteins found to be essential to insect viability can be recombinantly produced through standard molecular biological techniques and utilized as insecticide targets in screens for novel inhibitors of the enzymes' activity. The novel inhibitors discovered through such screens may then be used as insecticides to control undesirable insect infestation.

However, as the world population continues to grow, there will be increasing food shortages. Therefore, there exists continuing need to find new, effective and economic insecticides.

SUMMARY OF THE INVENTION

In view of these needs, it is one object of the invention to provide essential genes in insects such as *Drosophila melanogaster*. It is another object to provide the essential proteins encoded by these essential genes for assay development to identify inhibitory compounds with insecticidal activity. It is still another object of the present invention to provide an effective and beneficial method for identifying new or improved insecticides using the essential proteins of the invention.

In furtherance of these and other objects, the present invention provides DNA molecules comprising nucleotide sequences isolated from *Drosophila melanogaster* that encode proteins essential for larval viability. The inventors are the first to demonstrate that the nucleotide sequences of the invention are essential for larval viability. This knowledge is exploited to provide novel insecticide modes of action. One advantage of the present

invention is that the proteins encoded by the essential nucleotide sequences provide the bases for assays designed to easily and rapidly identify novel insecticides.

Disruption of the nucleotide sequences of the invention demonstrates that the activity of each corresponding encoded protein is essential for *Drosophila* larval viability. Genetic results show that when each nucleotide sequence of the invention is mutated in *Drosophila*, the resulting phenotype is larval lethal in the homozygous state. This demonstrates a critical role for the protein encoded by the mutated nucleotide sequence. This further implies that chemicals that inhibit the expression of the protein when in contact with insects are likely to have detrimental effects on insects and are potentially good insecticide candidates. The present invention therefore provides methods of using the disclosed nucleotide sequences or proteins encoded thereby to identify inhibitors thereof. The inhibitors can then be used as insecticides to kill undesirable insect populations where crops are grown, particularly agronomically important crops such as maize, and other cereal crops such as wheat, oats, rye, sorgum, rice, barley, millet, turf and forage grasses and the like, as well as cotton, sugar cane, sugar beet, oilseed rape, soybeans, vegetable crops and fruits.

The present invention accordingly provides cDNA sequences derived from *Drosophila melanogaster*. In one embodiment, the present invention provides an isolated DNA molecule comprising a nucleotide sequence selected from the group consisting of the odd numbered SEQ ID NOs:1-73. In another embodiment, the present invention provides an isolated DNA molecule comprising a nucleotide sequence that encodes a protein selected from the group consisting of the even numbered SEQ ID NOs:2-74.

The present invention also provides a chimeric construct comprising a promoter operatively linked to a DNA molecule according to the present invention, wherein the promoter is preferably functional in a eukaryote, wherein the promoter is preferably heterologous to the DNA molecule. The present invention further provides a recombinant vector comprising a chimeric construct according to the present invention, wherein said vector is capable of being stably transformed into a host cell. The present invention still further provides a host cell comprising a DNA molecule according to the present invention, wherein said DNA molecule is preferably expressible in the cell. The host cell is preferably selected from the group consisting of an insect cell, a yeast cell, and a prokaryotic cell.

The present invention also provides proteins essential for *Drosophila melanogaster* larval viability. In one embodiment, the present invention provides an isolated protein comprising an amino acid sequence selected from the group consisting of the even numbered

SEQ ID NOs:2-74. In accordance with another embodiment, the present invention also relates to the recombinant production of proteins of the invention and methods of using the proteins of the invention in assays for identifying compounds that interact with the protein.

In another preferred embodiment, the present invention describes a method for identifying chemicals having the ability to inhibit the activity of the disclosed proteins. In a preferred embodiment, the present invention provides a method for selecting compounds that interact with a protein of the invention, comprising: (a) expressing a DNA molecule according to the present invention to generate the corresponding protein of the invention, (b) testing a compound suspected of having the ability to interact with the protein expressed in step (a), and (c) selecting compounds that interact with the protein in step (b).

Other objects and advantages of the present invention will become apparent to those skilled in the art and from a study of the following description of the invention and non-limiting examples. The entire contents of all publications mentioned herein are hereby incorporated by reference.

BRIEF DESCRIPTION OF THE SEQUENCES IN THE SEQUENCE LISTING

Odd numbered SEQ ID NOs:1-73 are nucleotide sequences described in the table below.

Even numbered SEQ ID NOs:2-74 are protein sequences encoded by the immediately preceding nucleotide sequence, e.g., SEQ ID NO:2 is the protein encoded by the nucleotide sequence of SEQ ID NO:1, SEQ ID NO:4 is the protein encoded by the nucleotide sequence of SEQ ID NO:3, etc.

SEQ ID NOs:75-87 are PCR primers.

SEQ ID NO:	CT	Gene Name	BLAST
1	CT10671		geminin L [Xenopus laevis] 4e-06
3	CT11789	SUH	Expect = 0 Score =735 gi|1477785 (U60093) suppressor of hairless protein 1 [Xenopus laevis]
5	CT12299		6016932 Expect = 1.e-110 Score =777 gi|6016932|emb|CAB57836.1| (AL031667) dJ620E11.1a (novel Helicase C-terminal domain and SNF2 N-termi
7	CT12433		F5M15.23 [Arabidopsis] 5e-11
9	CT13750	NOT	KIAA1063 protein [Homo sapiens] e-137
11	CT14668		Expect = 1.e-06 Score =56.2 gi|4008434|emb|CAA21644.1| (AL032640) predicted using Genefinder; cDNA EST yk416g4.5 comes from this
13	CT14840		gi|5051628|gb|AAD38322.1|AF047033_1 (AF047033) sodium bicarbonate cotransporter 3 [Homo sapiens]
15	CT14856		gi|7503817|pir||T22427 hypothetical protein F49C5.4 - Caenorhabditis elegans >gi|3877329|emb|CAB04433.1| (Z81544) contains similarity to Pfam domain: PF00069 (Eukaryotic protein kinase domain), Score=306.1,E-value=1.4e-88, N=1 [Caenorhabditis elegans] Score = 277 bits (702), Expect = 2e-73
17	CT1649		Y09022 g1653999 Human mRNA for Not56-like protein.
19	CT17906		M. musculus 1168457 Expect = 1.e-24 Score =415.7 gi|1168457|sp|Q02357|ANK1_MOUSE ANKYRIN >gi|2119259|pir||I49502 ankyrin - mouse >gi|191940 (M84756)
21	CT18206		synaptotagmin 5 [Homo sapiens] 2.3
23	CT19380		
25	CT19738	TARA	
27	CT20428	CNK	Expect = 2.e-47 Score =264.2 gi|4151807|gb|AAD04568.1| (AF102854) membrane-associated guanylate kinase-interacting protein 2 Magu
29	CT20708	AGO1	C. elegans 3877299 Expect = 0 Score =1256 gi|3877299|emb|CAA93496.1| (Z69661) cDNA EST EMBL:D70203 comes from this gene; cDNA EST EMBL:D71003
31	CT21945	DUP	gi|7573546|emb|CAB87836.1| (AJ250122) putative CDT1 protein [Xenopus laevis] Score = 241 bits (609), Expect = 2e-62
33	CT22383	GLYP	Expect = 0 Score =1252 gi|1836054|bbs|179296 (S82859) alpha-1,4-glucan orthophosphate glycosyl transferase, myophosphorylas
35	CT22943	OSA	SWI1Lbeta protein [Homo sapiens] 2e-72
37	CT23155	MCR	KIAA1283 protein [Homo sapiens] 9e-05
39	CT23802		Expect = 1.e-118 Score = 425 gi|2645879 (AF034374) molybdenum cofactor biosynthesis protein A [Homo sapiens]
41	CT2428		Expect = 7.e-24 Score =186.6 gi|3878582|emb|CAB01235.1| (Z77667) predicted using

43	CT25884		Genefinder; similar to zinc-finger protein; cDNA gi|6648069|sp|P50544|ACDV_MOUSE ACYL-COA DEHYDROGENASE, VERY-LONG-CHAIN SPECIFIC,MITOCHONDRIAL PREC
45	CT26690	XBP1	Remainders 2118500 Expect = 7.e-12 Score =73.4 gi|2118500|pir||JC4857 hepatocarcinogenesis-related transcription factor - rat >gi|5596360|dbj|BAA82
47	CT27692		Expect = 2.e-16 Score =87.4 gi|465731|sp|P34276|YKJ2_CAEEL HYPOTHETICAL 36.9 KD PROTEIN C02D5.2 IN CHROMOSOME III >gi|630504|pir , 1.e-05 51.5 gi|5453696|ref|NP_006323.1|| interferon, gamma-inducible protein 30 >gi|124495|sp|P13284|INIP_HUMAN
49	CT28625	NOP5	H. sapiens 4680298 Expect = 1.e-Score =144 535.9 gi|4680298|gb|AAD27610.1|AF123534_1 (AF123534) nucleolar protein NOP5/NOP58 [Homo sapiens]
51	CT28865	HOW	C. elegans 1947005 Expect =5.e-75 Score =282 gi|1947005 (AF000197) similar to C. elegans female germline-specific tumor suppressor GLD-1 (SP:G841
53	CT29244		Sil1 protein [Mus musculus] 7e-31
55	CT29824	RPL30	Expect =4.e-45 Score =180 gi|4506631|ref|NP_000980.1|| ribosomal protein L30 >gi|6677783|ref|NP_033109.1|| ribosomal protein L
57	CT34960		
59	CT36603	Ubi-p63E	Expect =1.e-21 Score =202 gi|84834|pir||JH0302 polyubiquitin - tobacco hornworm (fragments)
61	CT37944		M. musculus 2494763 Expect =0 Score =783 gi|2494763|sp|P70698|PYRG_MOUSE CTP SYNTHASE (UTP--AMMONIA LIGASE) (CTP SYNTHETASE) >gi|1515357 (U49 H. sapiens 4503133 0 783 gi|4503133|ref|NP_001896.1|| CTP synthase; cytidine 5-prime triphosphate synthetase >gi|131735|sp|P1
63	CT38280	SNF4A&GGR	AMP-activated protein kinase gamma2 subunit [Homo sapiens] e-110
65	CT9393	BcDNA:GH08860	Expect =5.e-86 319 gi|730984|sp|P40387|TPS1_SCHPO ALPHA,ALPHA-TREHALOSE-PHOSPHATE SYNTHASE [UDP-FORMING] (TREHALOSE-6-P
67	GH22170		2.4 Y16752 g3757660 Human mRNA for secretagogin, complete cds. 0
69	GM02843		9 AF047437 g3335129 Human sperm acrosomal protein mRNA, complete cds. 0
71	GM03018		0.03 MATERNAL PUMILIO PROTEIN >gi|103349|pir||S22026 pumilio protein - fruit fly (Drosophila melanogaster) >gi|8394|emb|CAA44474| (X62589) pumilio [Drosophila melanogaster]
73	UNI1	UNI1	

DEFINITIONS

For clarity, certain terms used in the specification are defined and used as follows:

"Associated with / operatively linked" refer to two nucleic acid sequences that are related physically or functionally. For example, a promoter or regulatory DNA sequence is said to be "associated with" a DNA sequence that codes for an RNA or a protein if the two sequences are operatively linked, or situated such that the regulator DNA sequence will affect the expression level of the coding or structural DNA sequence.

A "chimeric construct" is a recombinant nucleic acid sequence in which a promoter or regulatory nucleic acid sequence is operatively linked to, or associated with, a nucleic acid sequence that codes for an mRNA or which is expressed as a protein, such that the regulatory nucleic acid sequence is able to regulate transcription or expression of the associated nucleic acid sequence. The regulatory nucleic acid sequence of the chimeric construct is not normally operatively linked to the associated nucleic acid sequence as found in nature.

Co-factor: natural reactant, such as an organic molecule or a metal ion, required in an enzyme-catalyzed reaction. A co-factor is e.g. NAD(P), riboflavin (including FAD and FMN), folate, molybdopterin, thiamin, biotin, lipoic acid, pantothenic acid and coenzyme A, S-adenosylmethionine, pyridoxal phosphate, ubiquinone, menaquinone. Optionally, a co-factor can be regenerated and reused.

A "coding sequence" is a nucleic acid sequence that is transcribed into RNA such as mRNA, rRNA, tRNA, snRNA, sense RNA or antisense RNA. Preferably the RNA is then translated in an organism to produce a protein.

Complementary: "complementary" refers to two nucleotide sequences that comprise antiparallel nucleotide sequences capable of pairing with one another upon formation of hydrogen bonds between the complementary base residues in the antiparallel nucleotide sequences.

"Conservatively modified variations" of a particular nucleic acid sequence refers to those nucleic acid sequences that encode identical or essentially identical amino acid sequences, or where the nucleic acid sequence does not encode an amino acid sequence, to essentially identical sequences. Because of the degeneracy of the genetic code, a large number of functionally identical nucleic acids encode any given polypeptide. For instance the codons CGT, CGC, CGA, CGG, AGA, and AGG all encode the amino acid arginine. Thus, at every position where an arginine is specified by a codon, the codon can be altered to any of the

corresponding codons described without altering the encoded protein. Such nucleic acid variations are "silent variations" which are one species of "conservatively modified variations." Every nucleic acid sequence described herein which encodes a protein also describes every possible silent variation, except where otherwise noted. One of skill will recognize that each codon in a nucleic acid (except ATG, which is ordinarily the only codon for methionine) can be modified to yield a functionally identical molecule by standard techniques. Accordingly, each "silent variation" of a nucleic acid which encodes a protein is implicit in each described sequence.

Furthermore, one of skill will recognize that individual substitutions deletions or additions that alter, add or delete a single amino acid or a small percentage of amino acids (typically less than 5%, more typically less than 1%) in an encoded sequence are "conservatively modified variations," where the alterations result in the substitution of an amino acid with a chemically similar amino acid. Conservative substitution tables providing functionally similar amino acids are well known in the art. The following five groups each contain amino acids that are conservative substitutions for one another: Aliphatic: Glycine (G), Alanine (A), Valine (V), Leucine (L), Isoleucine (I); Aromatic: Phenylalanine (F), Tyrosine (Y), Tryptophan (W); Sulfur-containing: Methionine (M), Cysteine (C); Basic: Arginine (R), Lysine (K), Histidine (H); Acidic: Aspartic acid (D), Glutamic acid (E), Asparagine (N), Glutamine (Q). *See also,* Creighton (1984) *Proteins, W.H.* Freeman and Company. In addition, individual substitutions, deletions or additions which alter, add or delete a single amino acid or a small percentage of amino acids in an encoded sequence are also "conservatively modified variations."

DNA Shuffling: DNA shuffling is a method to rapidly, easily and efficiently introduce mutations or rearrangements, preferably randomly, in a DNA molecule or to generate exchanges of DNA sequences between two or more DNA molecules, preferably randomly. The DNA molecule resulting from DNA shuffling is a shuffled DNA molecule that is a non-naturally occurring DNA molecule derived from at least one template DNA molecule. The shuffled DNA encodes an enzyme modified with respect to the enzyme encoded by the template DNA, and preferably has an altered biological activity with respect to the enzyme encoded by the template DNA.

Enzyme/Protein Activity: means herein the ability of an enzyme (or protein) to catalyze the conversion of a substrate into a product. A substrate for the enzyme comprises the natural substrate of the enzyme but also comprises analogues of the natural substrate, which can also

be converted, by the enzyme into a product or into an analogue of a product. The activity of the enzyme is measured for example by determining the amount of product in the reaction after a certain period of time, or by determining the amount of substrate remaining in the reaction mixture after a certain period of time. The activity of the enzyme is also measured by determining the amount of an unused co-factor of the reaction remaining in the reaction mixture after a certain period of time or by determining the amount of used co-factor in the reaction mixture after a certain period of time. The activity of the enzyme is also measured by determining the amount of a donor of free energy or energy-rich molecule (e.g. ATP, phosphoenolpyruvate, acetyl phosphate or phosphocreatine) remaining in the reaction mixture after a certain period of time or by determining the amount of a used donor of free energy or energy-rich molecule (e.g. ADP, pyruvate, acetate or creatine) in the reaction mixture after a certain period of time.

Essential: an "essential" *Drosophila melanogaster* nucleotide sequence is a nucleotide sequence encoding a protein such as e.g. a biosynthetic enzyme, receptor, signal transduction protein, structural gene product, or transport protein that is essential to the growth or survival of the insect.

Expression Cassette: "Expression cassette" as used herein means a DNA sequence capable of directing expression of a particular nucleotide sequence in an appropriate host cell, comprising a promoter operatively linked to the nucleotide sequence of interest which is operatively linked to termination signals. It also typically comprises sequences required for proper translation of the nucleotide sequence. The coding region usually codes for a protein of interest but may also code for a functional RNA of interest, for example antisense RNA or a nontranslated RNA, in the sense or antisense direction. The expression cassette comprising the nucleotide sequence of interest may be chimeric, meaning that at least one of its components is heterologous with respect to at least one of its other components. The expression cassette may also be one which is naturally occurring but has been obtained in a recombinant form useful for heterologous expression. Typically, however, the expression cassette is heterologous with respect to the host, i.e., the particular DNA sequence of the expression cassette does not occur naturally in the host cell and must have been introduced into the host cell or an ancestor of the host cell by a transformation event. The expression of the nucleotide sequence in the expression cassette may be under the control of a constitutive promoter or of an inducible promoter which initiates transcription only when the host cell is exposed to some particular external stimulus. In the case of a multicellular organism, such as

an insect, the promoter can also be specific to a particular tissue or organ or stage of development.

Gene: the term "gene" is used broadly to refer to any segment of DNA associated with a biological function. Thus, genes include coding sequences and/or the regulatory sequences required for their expression. Genes also include nonexpressed DNA segments that, for example, form recognition sequences for other proteins. Genes can be obtained from a variety of sources, including cloning from a source of interest or synthesizing from known or predicted sequence information, and may include sequences designed to have desired parameters.

Heterologous/exogenous: The terms "heterologous" and "exogenous" when used herein to refer to a nucleic acid sequence (e.g. a DNA sequence) or a gene, refer to a sequence that originates from a source foreign to the particular host cell or, if from the same source, is modified from its original form. Thus, a heterologous gene in a host cell includes a gene that is endogenous to the particular host cell but has been modified through, for example, the use of DNA shuffling. The terms also include non-naturally occurring multiple copies of a naturally occurring DNA sequence. Thus, the terms refer to a DNA segment that is foreign or heterologous to the cell, or homologous to the cell but in a position within the host cell nucleic acid in which the element is not ordinarily found. Exogenous DNA segments are expressed to yield exogenous polypeptides.

A "homologous" nucleic acid (e.g. DNA) sequence is a nucleic acid (e.g. DNA) sequence naturally associated with a host cell into which it is introduced.

The terms "identical" or percent "identity" in the context of two or more nucleic acid or protein sequences, refer to two or more sequences or subsequences that are the same or have a specified percentage of amino acid residues or nucleotides that are the same, when compared and aligned for maximum correspondence, as measured using one of the following sequence comparison algorithms or by visual inspection.

Inhibitor: a chemical substance that inactivates the enzymatic activity of an enzyme (or protein) of interest. The term "insecticide" is used herein to define an inhibitor when applied to an insect at any stage of development.

Insecticide: a chemical substance used to kill or inhibit the growth or viability of insects at any stage of development.

Interaction: quality or state of mutual action such that the effectiveness or toxicity of one protein or compound on another protein is inhibitory (antagonists) or enhancing (agonists).

A nucleic acid sequence is "isocoding with" a reference nucleic acid sequence when the nucleic acid sequence encodes a polypeptide having the same amino acid sequence as the polypeptide encoded by the reference nucleic acid sequence.

An "isolated" nucleic acid molecule or an isolated enzyme is a nucleic acid molecule or enzyme that, by the hand of man, exists apart from its native environment and is therefore not a product of nature. An isolated nucleic acid molecule or enzyme may exist in a purified form or may exist in a non-native environment such as, for example, a recombinant host cell.

Mature Protein: protein that is normally targeted to a cellular organelle and from which the transit peptide has been removed.

Minimal Promoter: promoter elements, particularly a TATA element, that are inactive or that have greatly reduced promoter activity in the absence of upstream activation. In the presence of a suitable transcription factor, the minimal promoter functions to permit transcription.

Modified Enzyme Activity: enzyme activity different from that which naturally occurs in an insect (i.e. enzyme activity that occurs naturally in the absence of direct or indirect manipulation of such activity by man), which is tolerant to inhibitors that inhibit the naturally occurring enzyme activity.

Native: refers to a gene that is present in the genome of an untransformed insect cell.

Naturally occurring: the term "naturally occurring" is used to describe an object that can be found in nature as distinct from being artificially produced by man. For example, a protein or nucleotide sequence present in an organism (including a virus), which can be isolated from a source in nature and which has not been intentionally modified by man in the laboratory, is naturally occurring.

Nucleic acid: the term "nucleic acid" refers to deoxyribonucleotides or ribonucleotides and polymers thereof in either single- or double-stranded form. Unless specifically limited, the term encompasses nucleic acids containing known analogues of natural nucleotides which have similar binding properties as the reference nucleic acid and are metabolized in a manner similar to naturally occurring nucleotides. Unless otherwise indicated, a particular nucleic acid sequence also implicitly encompasses conservatively modified variants thereof *(e.g.* degenerate codon substitutions) and complementary sequences and as well as the sequence

explicitly indicated. Specifically, degenerate codon substitutions may be achieved by generating sequences in which the third position of one or more selected (or all) codons is substituted with mixed-base and/or deoxyinosine residues (Batzer *et al., Nucleic Acid Res.* 19: 5081 (1991); Ohtsuka *et al., J. Biol. Chem.* 260: 2605-2608 (1985); Rossolini *et al., Mol. Cell. Probes* 8: 91-98 (1994)). The terms "nucleic acid" or "nucleic acid sequence" may also be used interchangeably with gene, cDNA, and mRNA encoded by a gene.

"ORF" means open reading frame.

Purified: the term "purified," when applied to a nucleic acid or protein, denotes that the nucleic acid or protein is essentially free of other cellular components with which it is associated in the natural state. It is preferably in a homogeneous state although it can be in either a dry or aqueous solution. Purity and homogeneity are typically determined using analytical chemistry techniques such as polyacrylamide gel electrophoresis or high performance liquid chromatography. A protein which is the predominant species present in a preparation is substantially purified. The term "purified" denotes that a nucleic acid or protein gives rise to essentially one band in an electrophoretic gel. Particularly, it means that the nucleic acid or protein is at least about 50% pure, more preferably at least about 85% pure, and most preferably at least about 99% pure.

Two nucleic acids are "recombined" when sequences from each of the two nucleic acids are combined in a progeny nucleic acid. Two sequences are "directly" recombined when both of the nucleic acids are substrates for recombination. Two sequences are "indirectly recombined" when the sequences are recombined using an intermediate such as a cross-over oligonucleotide. For indirect recombination, no more than one of the sequences is an actual substrate for recombination, and in some cases, neither sequence is a substrate for recombination.

"Regulatory elements" refer to sequences involved in controlling the expression of a nucleotide sequence. Regulatory elements comprise a promoter operatively linked to the nucleotide sequence of interest and termination signals. They also typically encompass sequences required for proper translation of the nucleotide sequence.

Significant Increase: an increase in enzymatic activity that is larger than the margin of error inherent in the measurement technique, preferably an increase by about 2-fold or greater of the activity of the wild-type enzyme in the presence of the inhibitor, more preferably an increase by about 5-fold or greater, and most preferably an increase by about 10-fold or greater.

Substantially identical: the phrase "substantially identical," in the context of two nucleic acid or protein sequences, refers to two or more sequences or subsequences that have at least 60%, preferably 80%, more preferably 90, even more preferably 95%, and most preferably at least 99% nucleotide or amino acid residue identity, when compared and aligned for maximum correspondence, as measured using one of the following sequence comparison algorithms or by visual inspection. Preferably, the substantial identity exists over a region of the sequences that is at least about 50 residues in length, more preferably over a region of at least about 100 residues, and most preferably the sequences are substantially identical over at least about 150 residues. In an especially preferred embodiment, the sequences are substantially identical over the entire length of the coding regions. Furthermore, substantially identical nucleic acid or protein sequences perform substantially the same function.

For sequence comparison, typically one sequence acts as a reference sequence to which test sequences are compared. When using a sequence comparison algorithm, test and reference sequences are input into a computer, subsequence coordinates are designated if necessary, and sequence algorithm program parameters are designated. The sequence comparison algorithm then calculates the percent sequence identity for the test sequence(s) relative to the reference sequence, based on the designated program parameters.

Optimal alignment of sequences for comparison can be conducted, e.g., by the local homology algorithm of Smith & Waterman, *Adv. Appl. Math.* 2: 482 (1981), by the homology alignment algorithm of Needleman & Wunsch, *J. Mol. Biol.* 48: 443 (1970), by the search for similarity method of Pearson & Lipman, *Proc. Nat'l. Acad. Sci. USA* 85: 2444 (1988), by computerized implementations of these algorithms (GAP, BESTFIT, FASTA, and TFASTA in the Wisconsin Genetics Software Package, Genetics Computer Group, 575 Science Dr., Madison, WI), or by visual inspection (*see generally,* Ausubel *et al., infra).*

One example of an algorithm that is suitable for determining percent sequence identity and sequence similarity is the BLAST algorithm, which is described in Altschul *et al., J. Mol. Biol.* 215: 403-410 (1990). Software for performing BLAST analyses is publicly available through the National Center for Biotechnology Information on the world wide web at ncbi.nlm.nih.gov/. This algorithm involves first identifying high scoring sequence pairs (HSPs) by identifying short words of length W in the query sequence, which either match or satisfy some positive-valued threshold score T when aligned with a word of the same length in a database sequence. T is referred to as the neighborhood word score threshold (Altschul *et al.*, 1990). These initial neighborhood word hits act as seeds for initiating searches to find

longer HSPs containing them. The word hits are then extended in both directions along each sequence for as far as the cumulative alignment score can be increased. Cumulative scores are calculated using, for nucleotide sequences, the parameters M (reward score for a pair of matching residues; always > 0) and N (penalty score for mismatching residues; always < 0). For amino acid sequences, a scoring matrix is used to calculate the cumulative score. Extension of the word hits in each direction are halted when the cumulative alignment score falls off by the quantity X from its maximum achieved value, the cumulative score goes to zero or below due to the accumulation of one or more negative-scoring residue alignments, or the end of either sequence is reached. The BLAST algorithm parameters W, T, and X determine the sensitivity and speed of the alignment. The BLASTN program (for nucleotide sequences) uses as defaults a wordlength (W) of 11, an expectation (E) of 10, a cutoff of 100, M=5, N=-4, and a comparison of both strands. For amino acid sequences, the BLASTP program uses as defaults a wordlength (W) of 3, an expectation (E) of 10, and the BLOSUM62 scoring matrix *(see* Henikoff & Henikoff, *Proc. Natl. Acad. Sci. USA* 89: 10915 (1989)).

In addition to calculating percent sequence identity, the BLAST algorithm also performs a statistical analysis of the similarity between two sequences *(see, e.g.,* Karlin & Altschul, *Proc. Nat'l. Acad. Sci. USA* 90: 5873-5787 (1993)). One measure of similarity provided by the BLAST algorithm is the smallest sum probability (P(N)), which provides an indication of the probability by which a match between two nucleotide or amino acid sequences would occur by chance. For example, a test nucleic acid sequence is considered similar to a reference sequence if the smallest sum probability in a comparison of the test nucleic acid sequence to the reference nucleic acid sequence is less than about 0.1, more preferably less than about 0.01, and most preferably less than about 0.001.

Another indication that two nucleic acid sequences are substantially identical is that the two molecules hybridize to each other under stringent conditions. The phrase "hybridizing specifically to" refers to the binding, duplexing, or hybridizing of a molecule only to a particular nucleotide sequence under stringent conditions when that sequence is present in a complex mixture (*e.g.,* total cellular) DNA or RNA. "Bind(s) substantially" refers to complementary hybridization between a probe nucleic acid and a target nucleic acid and embraces minor mismatches that can be accommodated by reducing the stringency of the hybridization media to achieve the desired detection of the target nucleic acid sequence.

"Stringent hybridization conditions" and "stringent hybridization wash conditions" in the context of nucleic acid hybridization experiments such as Southern and Northern hybridizations are sequence dependent, and are different under different environmental parameters. Longer sequences hybridize specifically at higher temperatures. An extensive guide to the hybridization of nucleic acids is found in Tijssen (1993) *Laboratory Techniques in Biochemistry and Molecular Biology-Hybridization with Nucleic* Acid Probes part I chapter 2 "Overview of principles of hybridization and the strategy of nucleic acid probe assays" Elsevier, New York. Generally, highly stringent hybridization and wash conditions are selected to be about 5°C lower than the thermal melting point (T_m) for the specific sequence at a defined ionic strength and pH. Typically, under "stringent conditions" a probe will hybridize to its target subsequence, but to no other sequences.

The T_m is the temperature (under defined ionic strength and pH) at which 50% of the target sequence hybridizes to a perfectly matched probe. Very stringent conditions are selected to be equal to the T_m for a particular probe. An example of stringent hybridization conditions for hybridization of complementary nucleic acids which have more than 100 complementary residues on a filter in a Southern or northern blot is 50% formamide with 1 mg of heparin at 42°C, with the hybridization being carried out overnight. An example of highly stringent wash conditions is 0.1 5M NaCl at 72°C for about 15 minutes. An example of stringent wash conditions is a 0.2x SSC wash at 65°C for 15 minutes (*see,* Sambrook, *infra,* for a description of SSC buffer). Often, a high stringency wash is preceded by a low stringency wash to remove background probe signal. An example medium stringency wash for a duplex of, e.g., more than 100 nucleotides, is 1x SSC at 45°C for 15 minutes. An example low stringency wash for a duplex of, *e.g.,* more than 100 nucleotides, is 4-6x SSC at 40°C for 15 minutes. For short probes (*e.g.,* about 10 to 50 nucleotides), stringent conditions typically involve salt concentrations of less than about 1.0 M Na ion, typically about 0.01 to 1.0 M Na ion concentration (or other salts) at pH 7.0 to 8.3, and the temperature is typically at least about 30°C. Stringent conditions can also be achieved with the addition of destabilizing agents such as formamide. In general, a signal to noise ratio of 2x (or higher) than that observed for an unrelated probe in the particular hybridization assay indicates detection of a specific hybridization. Nucleic acids that do not hybridize to each other under stringent conditions are still substantially identical if the proteins that they encode are substantially identical. This occurs, e.g., when a copy of a nucleic acid is created using the maximum codon degeneracy permitted by the genetic code.

The following are examples of sets of hybridization/wash conditions that may be used to clone homologous nucleotide sequences that are substantially identical to reference nucleotide sequences of the present invention: a reference nucleotide sequence preferably hybridizes to the reference nucleotide sequence in 7% sodium dodecyl sulfate (SDS), 0.5 M $NaPO_4$, 1 mM EDTA at 50°C with washing in 2X SSC, 0.1% SDS at 50°C, more desirably in 7% sodium dodecyl sulfate (SDS), 0.5 M $NaPO_4$, 1 mM EDTA at 50°C with washing in 1X SSC, 0.1% SDS at 50°C, more desirably still in 7% sodium dodecyl sulfate (SDS), 0.5 M $NaPO_4$, 1 mM EDTA at 50°C with washing in 0.5X SSC, 0.1% SDS at 50°C, preferably in 7% sodium dodecyl sulfate (SDS), 0.5 M $NaPO_4$, 1 mM EDTA at 50°C with washing in 0.1X SSC, 0.1% SDS at 50°C, more preferably in 7% sodium dodecyl sulfate (SDS), 0.5 M $NaPO_4$, 1 mM EDTA at 50°C with washing in 0.1X SSC, 0.1% SDS at 65°C.

A further indication that two nucleic acid sequences or proteins are substantially identical is that the protein encoded by the first nucleic acid is immunologically cross reactive with, or specifically binds to, the protein encoded by the second nucleic acid. Thus, a protein is typically substantially identical to a second protein, for example, where the two proteins differ only by conservative substitutions.

The phrase "specifically (or selectively) binds to an antibody," or "specifically (or selectively) immunoreactive with," when referring to a protein or peptide, refers to a binding reaction which is determinative of the presence of the protein in the presence of a heterogeneous population of proteins and other biologics. Thus, under designated immunoassay conditions, the specified antibodies bind to a particular protein and do not bind in a significant amount to other proteins present in the sample. Specific binding to an antibody under such conditions may require an antibody that is selected for its specificity for a particular protein. For example, antibodies raised to the protein with the amino acid sequence encoded by any of the nucleic acid sequences of the invention can be selected to obtain antibodies specifically immunoreactive with that protein and not with other proteins except for polymorphic variants. A variety of immunoassay formats may be used to select antibodies specifically immunoreactive with a particular protein. For example, solid-phase ELISA immunoassays, Western blots, or immunohistochemistry are routinely used to select monoclonal antibodies specifically immunoreactive with a protein. See Harlow and Lane (1988) *Antibodies, A Laboratory Manual,* Cold Spring Harbor Publications, New York "Harlow and Lane"), for a description of immunoassay formats and conditions that can be used to determine specific immunoreactivity. Typically a specific or selective reaction will be

at least twice background signal or noise and more typically more than 10 to 100 times background.

A "subsequence" refers to a sequence of nucleic acids or amino acids that comprise a part of a longer sequence of nucleic acids or amino acids (e.g., protein) respectively.

"Synthetic" refers to a nucleotide sequence comprising structural characters that are not present in the natural sequence. For example, an artificial sequence that resembles more closely the G+C content and the normal codon distribution of dicot and/or monocot genes is said to be synthetic.

Substrate: a substrate is the molecule that an enzyme naturally recognizes and converts to a product in the biochemical pathway in which the enzyme naturally carries out its function, or is a modified version of the molecule, which is also recognized by the enzyme and is converted by the enzyme to a product in an enzymatic reaction similar to the naturally-occurring reaction.

Target gene: A "target gene" is any gene in an insect cell. For example, a target gene is a gene of known function or is a gene whose function is unknown, but whose total or partial nucleotide sequence is known. Alternatively, the function of a target gene and its nucleotide sequence are both unknown. A target gene is a native gene of the insect cell or is a heterologous gene that had previously been introduced into the insect cell or a parent cell of said insect cell, for example by genetic transformation. A heterologous target gene is stably integrated in the genome of the insect cell or is present in the insect cell as an extrachromosomal molecule, e.g. as an autonomously replicating extrachromosomal molecule.

Transformation: a process for introducing heterologous DNA into a cell, tissue, or insect. Transformed cells, tissues, or insects are understood to encompass not only the end product of a transformation process, but also transgenic progeny thereof.

"Transformed," "transgenic," and "recombinant" refer to a host organism such as a bacterium or a plant into which a heterologous nucleic acid molecule has been introduced. The nucleic acid molecule can be stably integrated into the genome of the host or the nucleic acid molecule can also be present as an extrachromosomal molecule. Such an extrachromosomal molecule can be auto-replicating. Transformed cells, tissues, or plants are understood to encompass not only the end product of a transformation process, but also transgenic progeny thereof. A "non-transformed," "non-transgenic," or "non-recombinant" host refers to a wild-type organism, e.g., a bacterium or plant, which does not contain the

heterologous nucleic acid molecule.

Viability: "viability" as used herein refers to a fitness parameter of an insect. Insects are assayed for their homozygous performance of *Drosophila* larval development, indicating which proteins are indispensable to maintain larval life in *Drosophila*.

DETAILED DESCRIPTION OF THE INVENTION

I. Identification Of Essential *Drosophila melanogaster* Nucleotide Sequences Using Transposable Element Insertion Mutagenesis

As shown in the examples below, the identification of novel nucleotide sequences, as well as the essentiality of the nucleotide sequences for normal insect viability, have been demonstrated in *Drosophila* using P-element transposable insertion mutagenesis. Having established the essentiality of the function of the encoded proteins in *Drosophila* and having identified the nucleotide sequences encoding these essential proteins, the inventors thereby provide an important and sought-after tool for new insecticide development.

A lethal phenotype caused by insertion of a P-element indicates that the affected nucleotide sequence codes for an essential protein in the insect. The characterization of the insertion site using flanking sequence DNA is needed to associate an individual larval lethal line with specific nucleotide sequences. Genomic DNA adjacent to the 5' and/or 3' end of the P-element from the insertion line is generated using inverse PCR.

II. Determining The Complete Coding Sequences Of The Essential *Drosophila* Nucleotide Sequences

The essential *Drosophila* nucleotide sequences are identified by isolating nucleotide sequences flanking the P-element insertion and aligning that sequence with genomic *Drosophila* sequence obtained from the Celera *Drosophila* database. The protein prediction for each genomic region is obtained by use of an exon algorithm program such as GeneMark. All exon algorithm programs currently used for prediction of proteins are susceptible to inaccuracies, including incomplete predictions of coding sequences, missing alternative splice variants, combining of nearby exons of adjacent genes, and mistranslation at intron-exon borders. The prediction of a complete coding sequence can be confirmed by several methods including polymerase chain reaction (PCR) amplification using the 5' and 3' sequence to verify the message, reverse transcription PCR (rtPCR) using an oligonucleotide internal

sequence to identify the 5' and/or 3' end, and screening of cDNA libraries from insect tissues with probes made from a particular sequence to isolate a true full-length clone. To confirm that the message size is accurate, a Northern blot can be hybridized with a probe from the nucleotide sequence. In addition, matches to the *Drosophila* EST database helps to confirm existence of message and gives information about the temporal and spatial pattern of expression. Mutation-causing P elements are known to preferentially cluster in the 5' region of affected genes (Spradling *et al., Proc. Natl. Acad. Sci. USA* 92: 10824-10830 (1995)), a tendency that increases the chance of recovering overlaps between short flanking sequences and 5' ESTs. The present invention therefore provides a number of essential nucleotide sequences as well as the amino acid sequences encoded thereby. cDNA clone sequences are set forth in odd numbered SEQ ID NOs:1-73. The corresponding encoded amino acid sequences are set forth in even numbered SEQ ID NOs:2-74.

The isolated gene sequences disclosed herein may be manipulated according to standard genetic engineering techniques to suit any desired purpose. For example, an entire *Drosophila* gene sequence or portions thereof may be used as a probe capable of specifically hybridizing to coding sequences and messenger RNAs. To achieve specific hybridization under a variety of conditions, such probes include, e.g. sequences that are unique among insect nucleotide sequences for a particular protein of interest and are at least 10 nucleotides in length, preferably at least 20 nucleotides in length, and most preferably at least 50 nucleotides in length. Such probes are used to amplify and analyze related nucleotide sequences from a chosen organism via PCR. This technique is useful to isolate additional insect nucleotide sequences from a desired organism or as a diagnostic assay to determine the presence of particular nucleotide sequences in an organism. This technique also is used to detect the presence of altered nucleotide sequences associated with a particular condition of interest such as insecticide tolerance, poor health, etc.

Gene-specific hybridization probes also are used to quantify levels of a particular gene mRNA in an insect using standard techniques such as Northern blot analysis. This technique is useful as a diagnostic assay to detect altered levels of gene expression that are associated with particular conditions such as enhanced tolerance to insecticides that target a particular gene.

III. Recombinant Production Of Protein And Uses Thereof

For recombinant production of a protein of the invention in a host organism, a nucleotide sequence encoding the protein is inserted into an expression cassette designed for the chosen host and introduced into the host where it is recombinantly produced. The choice of the specific regulatory sequences such as promoter, signal sequence, 5' and 3' untranslated sequence, and enhancer appropriate for the chosen host is within the level of the skill of the routineer in the art. The resultant molecule, containing the individual elements linking in the proper reading frame, is inserted into a vector capable of being transformed into the host cell. Suitable expression vectors and methods for recombinant production of proteins are well known for host organisms such as *E. coli*, yeast, and insect cells (see, e.g., Lucknow and Summers, *Bio/Technol.* 6:47 (1988)). Additional suitable expression vectors are baculovirus expression vectors, e.g., those derived from the genome of *Autographica californica* nuclear polyhedrosis virus (AcMNPV). A preferred baculovirus/insect system is PVL1392(3) used to transfect *Spodoptera frugiperda* SF9 cells (ATCC) in the presence of linear *Autographica californica* baculovirus DNA (Phramingen, San Diego, CA). The resulting virus is used to infect HighFive *Tricoplusia ni* cells (Invitrogen, La Jolla, CA).

Recombinantly produced proteins are isolated and purified using a variety of standard techniques. The actual techniques used vary depending upon the host organism used, whether the protein is designed for secretion, and other such factors. Such techniques are well known to the skilled artisan (*see, e.g.* chapter 16 of Ausubel, F. *et al.*, "Current Protocols in Molecular Biology", pub. by John Wiley & Sons, Inc. (1994).

IV. Assays For Characterizing The Proteins

Recombinantly produced proteins are useful for a variety of purposes. For example, they can be used in *in vitro* assays to screen known insecticidal chemicals whose target has not been identified to determine if they inhibit protein activity. Such *in vitro* assays may also be used as more general screens to identify chemicals that inhibit such protein activity and that are therefore novel insecticide candidates. Recombinantly produced proteins may also be used to elucidate the complex structure of these molecules and to further characterize their association with known inhibitors in order to rationally design new inhibitory insecticides. Alternatively, the recombinant protein can be used to isolate antibodies or peptides that modulate the activity and are useful in transgenic solutions.

V. *In vivo* Inhibitor Assay: Discovery of Small Molecule Ligands That Interact with Proteins Of Unknown Function.

Having identified a protein as a potential insecticide target based on its essentiality for insect larval viability, a next step is to develop an assay that allows screening large numbers of chemicals to determine which ones interact with the protein. Although it is straightforward to develop assays for proteins of known function, developing assays with proteins of unknown functions can be more difficult.

To address this issue, novel technologies are used that can detect interactions between a protein and a ligand without knowing the biological function of the protein. A short description of three methods is presented, including fluorescence correlation spectroscopy, surface-enhanced laser desorption/ionization, and biacore technologies. In addition to those descibed here, there are additional methods that are currently being developed that are also amenable to automated, large-scale screening.

Fluorescence Correlation Spectroscopy (FCS) theory was developed in 1972 but it is only in recent years that the technology to perform FCS became available (Madge et al. (1972) *Phys. Rev. Lett.*, 29: 705-708; Maiti et al. (1997) *Proc. Natl. Acad. Sci. USA*, 94: 11753-11757). FCS measures the average diffusion rate of a fluorescent molecule within a small sample volume. The sample size can be as low as 10^3 fluorescent molecules and the sample volume as low as the cytoplasm of a single bacterium. The diffusion rate is a function of the mass of the molecule and decreases as the mass increases. FCS can therefore be applied to protein-ligand interaction analysis by measuring the change in mass and therefore in diffusion rate of a molecule upon binding. In a typical experiment, the target to be analyzed is expressed as a recombinant protein with a sequence tag, such as a poly-histidine sequence, inserted at the N- or C-terminus. The expression takes place in *E. coli*, yeast or insect cells. The protein is purified by chromatography. For example, the poly-histidine tag can be used to bind the expressed protein to a metal chelate column such as Ni2+ chelated on iminodiacetic acid agarose. The protein is then labeled with a fluorescent tag such as carboxytetramethylrhodamine or BODIPY® (Molecular Probes, Eugene, OR). The protein is then exposed in solution to the potential ligand, and its diffusion rate is determined by FCS using instrumentation available from Carl Zeiss, Inc. (Thornwood, NY). Ligand binding is determined by changes in the diffusion rate of the protein.

Surface-Enhanced Laser Desorption/Ionization (SELDI) was invented by Hutchens and Yip during the late 1980's (Hutchens and Yip (1993) *Rapid Commun. Mass Spectrom.* 7: 576-

580). When coupled to a time-of-flight mass spectrometer (TOF), SELDI provides means to rapidly analyze molecules retained on a chip. It can be applied to ligand-protein interaction analysis by covalently binding the target protein on the chip and analyze by MS the small molecules that bind to this protein (Worrall et al. (1998) *Anal. Biochem.* 70: 750-756). In a typical experiment, the target to be analyzed is expressed as described for FCS. The purified protein is then used in the assay without further preparation. It is bound to the SELDI chip either by utilizing the poly-histidine tag or by other interaction such as ion exchange or hydrophobic interaction. The chip thus prepared is then exposed to the potential ligand via, for example, a delivery system able to pipet the ligands in a sequential manner (autosampler). The chip is then submitted to washes of increasing stringency, for example a series of washes with buffer solutions containing an increasing ionic strength. After each wash, the bound material is analyzed by submitting the chip to SELDI-TOF. Ligands that specifically bind the target will be identified by the stringency of the wash needed to elute them.

Biacore relies on changes in the refractive index at the surface layer upon binding of a ligand to a protein immobilized on the layer. In this system, a collection of small ligands is injected sequentially in a 2-5 microlitre cell with the immobilized protein. Binding is detected by surface plasmon resonance (SPR) by recording laser light refracting from the surface. In general, the refractive index change for a given change of mass concentration at the surface layer is practically the same for all proteins and peptides, allowing a single method to be applicable for any protein (Liedberg et al. (1983) *Sensors Actuators* 4: 299-304; Malmquist (1993) *Nature* 361: 186-187). In a typical experiment, the target to be analyzed is expressed as described for FCS. The purified protein is then used in the assay without further preparation. It is bound to the Biacore chip either by utilizing the poly-histidine tag or by other interaction such as ion exchange or hydrophobic interaction. The chip thus prepared is then exposed to the potential ligand via the delivery system incorporated in the instruments sold by Biacore (Uppsala, Sweden) to pipet the ligands in a sequential manner (autosampler). The SPR signal on the chip is recorded and changes in the refractive index indicate an interaction between the immobilized target and the ligand. Analysis of the signal kinetics on rate and off rate allows the discrimination between non-specific and specific interaction.

The compounds that are active in the methods disclosed herein may be used to combat agricultural pests such as aphids, locusts, spider mites, and boll weavils as well as such insect pests which attack stored grains and against immature stages of insects living on plant tissue.

The compounds are also useful as a nematodicide for the control of agriculturally important soil nematodes and plant parasites.

VI. Production of peptides

Phage particles displaying diverse peptide libraries permits rapid library construction, affinity selection, amplification and selection of ligands directed against an essential protein (H.B. Lowman, *Annu. Rev. Biophys. Biomol. Struct.* 26, 401-424 (1997)). Structural analysis of these selectants can provide new information about ligand-target molecule interactions and then in the process also provide a novel molecule that can enable the development of new insecticides based upon these peptides as leads.

The invention will be further described by reference to the following detailed examples. These examples are provided for purposes of illustration only, and are not intended to be limiting unless otherwise specified.

EXAMPLES

Standard recombinant DNA and molecular cloning techniques used here are well known in the art and are described by Sambrook, *et al.*, *Molecular Cloning*, eds., Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY (1989) and by T.J. Silhavy, M.L. Berman, and L.W. Enquist, *Experiments with Gene Fusions*, Cold Spring Harbor Laboratory, Cold Spring Harbor, NY (1984) and by Ausubel, F.M. *et al., Current Protocols in Molecular Biology*, pub. by Greene Publishing Assoc. and Wiley-Interscience (1987). Well known *Drosophila* molecular genetics techniques can be found, for example, in Robert, D.B., *Drosophila, A Practical Approach* (IRL Press, Washington, DC, 1986).

Example 1: Identification Of Larval Lethal Lines

Essential nucleotide sequences are identified through the isolation of lethal mutants defective in larval development. The genetic scheme for mobilization of P-lacW is as performed in Deak *et. al, Genetics* 147: 1697-1722 (1997). Additional larval lethal lines are identified and disclosed in Braun, A., B. Lemaitre, *et al., Genetics* 147: 623-634 (1997); Galloni, M. and B. A. Edgar, *Development* 126: 2365-2375 (1999); Gateff, E., *Int. J. Dev. Biol.* 38(4): 565-590 (1994); Mechler, B. M. J. Biosci., *Bangalore* 19(5): 537-556 (1994);

Roch, F., F. Serras, *et al., Mol. Gen. Genet.* 257: 103-112 (1998); Russell, M. A., L. Ostafichuk, *et al., Genome* 41: 7-13 (1998); and in Torok, T., G. Tick, *et al. Genetics* 135: 71-80 (1993). Furthermore, the BDGP gene disruption project of single P-element insertions reveals larval lethal lines mutating 25% of vital *Drosophila* genes Spradling, A. C., D. Stern, *et al., Genetics* 153: 135-177 (1999).

Males carrying the transposase source P(Δ2-3) are crossed en masse to yellow white females homozygous for a P-lacW insertion on the X chromosome. Males carrying the PlacW insertion on the X and Δ2-3 on the third chromosome are collected from this cross. The F0 "jumpstart" males are crossed in groups of 10-15 to 20-25 females of w spl; Sb/TM3, Ser genetype. Male F1 progeny with pigmented eyes indicate that the P-lacW has jumped to an autosome. An average of 10-15 males from each F0 cross lacking Δ2-3 are crossed individually to y w; DTS-4/TM3, Sb Ser females, that all third chromosomal insertions result in balanced F2 stocks. Insertions on other autosomes yield white-eyed flies in the F2 generation and are eliminated. The balanced third chromosome insertions are tested for lethality in the next generation by placing four to six pairs of y w; P-lacW/TM3, Sb Ser flies in a vial and examining their progeny for the presence of homozygous P-lacW flies. To analyze the lethal phase, the TM3, Sb Ser balancer is replaced by the TM6C, TB Sb chromosome. In such a genetic background, homozygous mutants can be identified by their wild-type body-length. An average of 10-15 pairs of flies are placed in vials supplemented with yeast paste, and the eggs are collected from each line for 1 day. The development of 50-100 progeny is monitored, and the presence of homozygotes are recorded in all developmental stages. Lethal phase is assigned to a developmental stage in which homozygote animals last appear. Larval lethal lines are identified and maintained.

Example 2: Sequence Determination

Inverse PCR: To determine the flanking sequence of the larval lethal lines, the "Inverse PCR and Cycle Sequencing Protocol for Recovery of Sequences Flanking PZ, PlacW, and PEP elements" of E. Jay Rehm, Berkeley *Drosophila* Genome Project on the world wide web at fruitfly.org/methods/ is used with slight modifications. These modifications include the following: genomic DNA is obtained from 10 flies, rather than 30 flies, with adjustments for final concentrations; all DNA precipitations are performed using glycogen; for some

Digest, End, Temperature	Forward PCR Primer	Reverse PCR Primer
H5h	Plac4	Plac1
H3h	Pry2	Pry1
H3l	Pry4	Plw3-1
M5h	Plac4	Plac1
M3h	Pry2	Pry1
M3l	Pry4	Plw3-1
S5h	Plac4	Plac1
S3h	Pry2	Pry1
S3l	Pry4	Plw3-1

PCR Primer Sequences (5' to 3'):

Plac4 (27)	- act gtg cgt tag gtc ctg ttc att gtt	SEQ ID NO:75
Plac1 (24)	- cac cca agg ctc tgc tcc cac aat	SEQ ID NO:76
Pry4 (23)	- caa tca tat cgc tgt ctc act ca	SEQ ID NO:77
Pry1 (26)	- cct tag cat gtc cgt ggg gtt tga at	SEQ ID NO:78
Pry2 (28)	- ctt gcc gac ggg acc acc tta tgt tat t	SEQ ID NO:79
Plw3-1 (19)	- tgt cgg cgt cat caa ctc c	SEQ ID NO:80
Pwht1 (19)	- gta acg cta atc act ccg aac agg tca ca	SEQ ID NO:81

Enzymatic Clean-Up for Sequencing: To 40 μl PCR reaction, add 4 μl of enzyme mix. Incubate at 37°C for 1 hour. Inactivate at 70°C for 10 minutes. (Enzyme Mix consists of 2.5U/μl Exonuclease I (Amersham E700732), 0.5U/μl Shrimp Alkaline Phosphatase (Amersham E70183), 1X Amplitaq PCR buffer, add dH_20 to final volume.)

Example 3: Sequence Analysis

Sequence of the flanking sequence generated by inverse PCR is performed on an ABI 3700 sequencer (Perkin Elmer) using BIG DYE sequencing reaction.

Primer sets for sequencing are as shown in the table below:

Digest, End, Temperature	Forward Primer	Reverse Primer
H5h	Splac2	Sp1
H3h	Pry2	Sp5
H3l	Spep1	Sp5
M5h	Splac2	Sp1
M3h	Pry2	Sp5
M3l	Spep1	Sp5
S5h	Splac2	Sp1
S3h	Pry2	Sp6
S3l	Spep1	Sp6

The following primer sets are designed to sequence both ends of PCR products recovered from PlacW and PZ strains:

Splac2 and Sp1 - for use with the Plac4/Plac1 5' PCR primer combination with either PZ or PlacW P-elements; allows sequencing of both ends of the PCR fragment.

Spep1 and Sp3 - for use with the Pry4/Pry1 3' PCR primer combination with PZ P-elements; allows sequencing of both ends of the PCR fragment.

Spep1 and Sp6 - for use with the Pry4/Plw3-1 3' PCR primer combination with PlacW P-elements where Sau3a digestion is performed; allows sequencing of both ends of the PCR fragment.

Spep1 and Sp5 - for use with the Pry4/Plw3-1 3' PCR primer combination where HinP1 digestion is performed; allows sequencing of both ends of the PCR fragment.

Pry1 and Pry2 – for use with the Pry1/Pry2 3' PCR primer combination; allows sequencing of both ends of the PCR fragment.

The PCR products recovered from PEP strains are sequenced with the following primers: Sp1- for use with the Pwht1/Plac1 5' PCR primer combination with the PEP element; Spep1- for use with the Pry4/Pry1 3' PCR primer combination with the PEP element; Pry1 and Pry2 for use with the Pry1/Pry2 3' PCR primer combination with the PEP element.

Primer Sequences (5' to 3'):

Splac2 (25)	- gaa ttc act ggc cgt cgt ttt aca a	SEQ ID NO:82
Sp1 (22)	- aca caa cct ttc ctc tca aca a	SEQ ID NO:83
Sp3 (24)	- gag tac gca aag ctt taa cta tgt	SEQ ID NO:84
Sp6 (23)	- tga cca cat cca aac atc ctc tt	SEQ ID NO:85
Sp5 (25)	- gca tca caa aaa tcg acg ctc aag t	SEQ ID NO:86
Spep1 (19)	- gac act cag aat act att c	SEQ ID NO:87

Melting temperatures of sequencing primers:

Splac2- 60.1°C

Sp1- 50.6°C

Sp3- 49.3°C

Sp6- 54.9°C

Sp5 -60.3°C

Spep1- 44.8°C

Example 4: Secondary Confirmation of Lethality

The lethality of the chromosome carrying the P-element insertion is demonstrated genetically as described in Example 1. The essential *Drosophila* nucleotide sequences are identified by isolating nucleotide sequences flanking the P-element insertion and aligning those sequences with genomic *Drosophila* sequence obtained from the Celera *Drosophila* database. However, in some instances, a second site mutation exists on the chromosome that is responsible for the lethality. In other instances, the location of the flanking sequence is such that determination of which gene(s) are affected by the P-element insertion is rendered difficult or impossible. Thus, to provide secondary confirmation that the gene indicated is essential, there are many methods that one skilled in the art can use, e.g., rescue of the lethality using transformation technology, perturbation of the gene in a targeted manner, or failure to complement a deficiency.

To provide secondary confirmation, larval lethal lines are crossed to a line containing a deficiency spanning the region of the insert. This creates a hemizygous condition in that particular region and reveals the recessive phenotype of the P-element. Complementation with deficiencies that unequivocally remove the P-element insertion site is taken as proof that the P-element does not cause the associated phenotype. Failure to complement indicates that

the strain is verified. This method is as performed in Spradling, A. C., D. Stern, *et al.*, *Genetics* 153: 135-177 (1999). While lines with secondary mutations closely linked to the P insertion might be erroneously verified by this procedure, further molecular and genetic analyses suggest that the frequency of such errors is small. RNA interference, described in Fire, A., S. Xu, *et al.*, *Nature* 391, 806-811 (1998) and Kennerdell, J.R. and Carthew, R.W., *Cell* 95, 1017-1026 (1998), is used as a method to target a gene of interest and demonstrate that the perturbation of the identified gene produces a lethal phenotype.

Example 5: Isolation Of Full Length cDNA

A cDNA screen is performed using a *Drosophila melanogaster* cDNA library probed with a portion of each nucleotide sequence disclosed in the Sequence Listing. Positive colonies are selected, a subset sequenced, and a clone corresponding to the full-length cDNA is recovered. Alternatively, primers from the predicted 5' and 3' end are used in polymerase chain reaction with either a *Drosophila* cDNA library or first strand cDNAs obtained by reverse transcription of *Drosophila* mRNAs as template to amplify a fragment representing the full-length clone.

Example 6: Expression Of Recombinant Protein In Insect Cells

Baculovirus vectors, which are derived from the genome of AcNPV virus, are designed to provide high levels of expression of cDNA in the SF9 line of insect cells (ATCC CRL# 1711). Recombinant baculovirus expressing the cDNA of the present invention is produced by the following standard methods (InVitrogen MaxBac Manual): cDNA constructs are ligated into the polyhedrin gene in a variety of baclovirus transfer vectors, including the pAC360 and the BleBAc vector (InVitrogen). Recombinant baculoviruses are generated by homologous recombination following co-transfection of the baculovirus transfer vector and linearized AcNPV genomic DNA (Kitts, P.A., *Nucleic Acid. Res.* 18: 5667 (1990)) into SF9 cells. Recombinant pAC360 viruses are identified by the absence of inclusion bodies in infected cells and recombinant pBlueBac viruses are identified on the basis of B-galactosidase expression (Summers, M.D. and Smith, G.E., Texas Agriculture Exp. Station Bulletin No. 1555). Following plaque purification, the *Drosophila* cDNA expression is measured.

The cDNA encoding the entire open reading frame for the *Drosophila* cDNA is inserted into the BamHI site of pBlueBacII. Constucts in the positive orientation, which are identified by sequence analysis, are used to transfect SF9 cells in the presence of linear AcNPV wild type DNA. Authentic, active *Drosophila* cDNA is found in the cytoplasm of infected cells. Active *Drosophila* cDNA is extracted from infected cells by hypotonic or detergent lysis.

Example 7: Expression Of Recombinant Protein In *E. coli*

A cDNA clone of the present invention is subcloned into an appropriate expression vector and transformed into *E. coli* using the manufacturer's conditions. Specific examples include plasmids such as pBluescript (Stratagene, La Jolla, CA), pFLAG (International Biotechnologies, Inc., New Haven, CT), and pTrcHis (Invitrogen, La Jolla, CA). *E. coli* is cultured, and expression of the recombinant protein is confirmed. Recombinant protein is then isolated using standard techniques.

Example 8: *In vitro* Binding Assays

Recombinant protein is obtained, for example according to Example 6 or Example 7. The protein is immobilized on chips appropriate for ligand binding assays. The protein immobilized on the chip is exposed to sample compound in solution according to methods well know in the art. While the sample compound is in contact with the immobilized protein measurements capable of detecting protein-ligand interactions are conducted. Examples of such measurements are SEDLI, biacore and FCS, described above. Compounds found to bind the protein are readily discovered in this fashion and are subjected to further characterization.

The above disclosed embodiments are illustrative. This disclosure of the invention will place one skilled in the art in possession of many variations of the invention. All such obvious and foreseeable variations are intended to be encompassed by the appended claims.

What is claimed is:

1. A method for identifying a compound that inhibits the activity of a protein essential for *Drosophila* larval viability, comprising:

(a) expressing in a recombinant host a DNA molecule comprising

(i) a nucleotide sequence selected from the group consisting of the odd numbered SEQ ID NOs:1-73, or

(ii) a nucleotide sequence encoding an amino acid sequence selected from the group consisting of the even numbered SEQ ID NOs:2-74,

to produce a protein essential for *Drosophila* larval viability;

(b) testing compounds suspected of having the ability to inhibit the activity of the protein expressed in (a); and

(c) identifying a compound tested in (b) that inhibits the activity of the protein.

2. A method for killing or inhibiting the growth or viability of an insect, comprising applying to the insect a compound identified according to the method of claim 1.

3. A method for identifying a compound that interacts with a protein essential for *Drosophila* larval viability, comprising:

(a) expressing in a recombinant host a DNA molecule comprising

(i) a nucleotide sequence selected from the group consisting of the odd numbered SEQ ID NOs:1-73, or

(ii) a nucleotide sequence encoding an amino acid sequence selected from the group consisting of the even numbered SEQ ID NOs:2-74,

to produce a protein essential for *Drosophila* larval viability;

(b) testing compounds suspected of having the ability to interact with the protein expressed in (a); and

(c) identifying a compound tested in (b) that interacts with the protein.

4. A method for killing or inhibiting the growth or viability of an insect, comprising applying to the insect a compound identified according to the method of claim 3.

5. A method for killing or inhibiting the growth or viability of an insect, comprising inhibiting expression in said insect of a protein having at least 60% sequence identity to an amino acid sequence selected from the group consisting of the even numbered SEQ ID NOs:2-74.

6. The method of claim 5, wherein expression of said protein is inhibited by disruption in said insect of a nucleotide sequence having at least 60% sequence identity to a nucleotide sequence selected from the group consisting of the odd numbered SEQ ID NOs:1-73.

7. The method of claim 6, wherein said nucleotide sequence is disrupted by RNA interference.

SEQUENCE LISTING

<110> Stam, Lynn
Bachmann, Jane
Broadus, Julie
Kamdar, Kim

<120> NUCLEIC ACID SEQUENCES FROM DROSOPHILA MELANOGASTER THAT ENCODE PROTEINS ESSENTIAL FOR LARVAL VIABILITY AND USES THEREOF

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cgggtcaagg agggagaaga atccgttaag aaggagaatg acgagaaaac agaagctgat 5580

atggaaaata agccagagcc cgtctttatc gatgtggagg agtactttgt gaaatatcgc 5640

aatttcagtt atctacattg cgagtggcga acagaagagg aactattaaa gggtgatcgc 5700

cgcgtagctg ctaagattcg tcgctttcag caaaagcagt ctcagcaatt gaatatattt 5760

gagaatatcg aagacgagcc cttcaaccag gactttactg aagtggatag agtgttagac 5820

atgtctgtgc atacagacga aaccagtgga gagactacga agcactacct ggtcaagtgg 5880

aagtcgcttc cctatgagga ttgcacttgg gagctagaag aagatgtaga taacgacaaa 5940

attgagcagt acctgcgctt taacaaaatc cctcaacgga gcgagtggaa gtctaaaaaa 6000

cgaccgcatc cagaattgtg gaaaaaactg gaaaagacgc ccgtctataa gggaggaaat 6060

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cacaactgca tactcgctga cgaaatgggc cttggaaaaa ctattcaaag tttgacattt 6180

gtgcactctg tatatgagta cggcattaga ggacctttct tagttatagc tcctctatct 6240

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agtggaaagg tattgaagga gcccatcaag tttaacgttt tgatcaccac ttttgaaatg 6420

atcgtgacag actacatgga cttaaaagcc tttaactggc gcctttgtgt gattgatgag 6480

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gagcacagag tattgctctc cggaactccc ctacaaaaca acatcagcga gctgttctcg 6600

ctgttaaact ttctggaacc ctcgcagttc tcctcacagg aagagttcat gtctgagttt 6660

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<210> 6
<211> 2237
<212> PRT
<213> Drosophila melanogaster

<400> 6

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20 25 30

Pro Pro Gly Gly Tyr Pro Pro Arg His Arg Pro Pro His Pro Leu Gln
35 40 45

Gln Gln Pro Gln Tyr Pro Ser Tyr Gln Pro Thr Ala Glu Asn Leu Tyr
50 55 60

Gly Leu Gly Ala Ala Asp His Gln Ala Ala Met Gly Leu Gly Val Gly
65 70 75 80

Val Gly Val Gly Ala Gly Met Gly Asp Leu Ser Gly Trp Gly Ala Ala
85 90 95

Pro Ser Val Pro Gly Gln Ala Ala Ala Tyr Pro Gly Ala Gly Leu Gly
100 105 110

Ala Tyr Gly His Pro Gln Ala Ala Pro Pro Ser Gln Gln Gln Arg Gln
115 120 125

Ser Asn Ala Ser Ala Tyr Arg Gln His Met Pro Ala Tyr Gly Gln Gln
130 135 140

Asp Gln Gln Lys Leu Ala Ser Tyr Gly Ala Gln Gln Ser Met Met Ala
145 150 155 160

Gly Tyr Gly Ser Leu Ala Pro Gln Gln Gln Gln Gln Gln Pro Pro
165 170 175

Thr Pro Gln Gln Gln Gln Gln Ala Gln Gln Val Gln Gln Gln Ala Gln

180 185 190

Gln Gln Gln Gln Gln Gln Gln Gln Ser Gln Gln Gln Ala Arg Leu
195 200 205

Pro Gln His Tyr Pro Gln Ala Pro Gly Gln His Pro Leu Tyr Pro Gly
210 215 220

Val Gly Ala Pro Thr Val Gln Ala Gly Gln Pro Pro Thr Pro Gln Ala
225 230 235 240

Tyr Ala His Ser Pro Tyr Gly Ser Pro Met Gln His Gln Pro Ser Arg
245 250 255

Gly Ala Pro Gln His Val Gly Tyr Gly His Thr Gly Leu Asp Gln Ala
260 265 270

Ser Ala Tyr Gly Gln His Val Pro Gly Gly Ala Pro Pro Gly His His
275 280 285

Leu Ser Ala Gln Gln Gln Gln Ala Ala Gln Gln Leu Gly Ala His Gln
290 295 300

Gln Gln Gln Leu Gln Ser Gln Gln Gln Gln Gln Ala Gln Gln Gln Gln
305 310 315 320

Pro His Val Ser Leu Met Gln Gln Gln Gln Leu Pro Gly Ala Gly Leu
325 330 335

Pro Pro Pro His Met Gly Met Pro Pro Ser Tyr Gly Ser His His Gln
340 345 350

Gln Gln Gln Gln Gln Gln Gln Thr Gln Gln Gln Gln Gln Gln Ser Ala
355 360 365

Pro Pro Tyr Met Ser Ser Ser Lys His Gln Gln Ala Ala Ala Gln Leu
370 375 380

Asn Ser Ser Pro Gln Tyr Arg Ala Pro Phe Pro Gln Leu Ser Pro Gln
385 390 395 400

Met Ser Pro Arg Pro Pro Thr Met Ser Pro His Pro Gln Met Ser Pro
405 410 415

Arg Pro Val Gly Val Ser Pro Ala Lys Pro Pro Pro Pro Gln Gln Gln
420 425 430

Gln Gln Gln Thr Gln Ala Gln Gln Pro Gln Gln Val Val Ser Asn Gln
435 440 445

Pro Ser Gln His Ser Ile Gln Gly Met Val Gly Leu Pro Ser Pro Arg
450 455 460

Pro Gln Pro Pro Thr Ser Gly Ala Gly Gly Ala Gly Ala Lys Gly Pro
465 470 475 480

Ala Pro Val Ala Ala Pro Val Asn Thr Leu Gln Ala Leu Glu Gln Met
485 490 495

Val Met Pro Ser Gln Ala Leu Gly Leu Pro Pro Met Asp Tyr Pro Ser
500 505 510

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Ala Tyr Arg Ser Ala Val Gly Pro Arg Met Pro Ala Ser Pro Gln Gln
        515                 520                 525

Gln Gln Gln Gln His Gln Gln Trp Gly Ala Ala His Gly Ala Gln His
    530                 535                 540

Leu Ala Ala Leu Gln Gln Gln Gln Ala Gln Gln Gln Gln Gln Gln Val
545                 550                 555                 560

Gln Gln Gln Gln Gln Ala Pro Pro Gln Gln Gln Gln Gln Ala Ala Met
                565                 570                 575

Leu Gln Ala Gln Gln Gln His His Gln Gln Gln Leu Ser Met Tyr Gly
            580                 585                 590

Gln Pro Met Gly Gln Gln Pro Gln Thr Ala Gln Gln Gln Val Val Pro
        595                 600                 605

Pro Val Thr Ser Gln Pro Pro Val Val Ala Ala Ser Gln Gln Gln Gln
    610                 615                 620

Gln Gln Gln His Gln Gln Gln Ser Leu Asn Asp Gln Leu Gln His Ser
625                 630                 635                 640

Ile Asn Asp Ile Val Gly Gly Gly Asn Ser Ser Gly Ala Thr Gly Gly
                645                 650                 655

Ala Gln Asn Gln His Gln Gln Gln Pro Gln Leu Ala Ala Met Ser Ser
            660                 665                 670

Pro Leu His Gln Gln Asn Leu Pro Asn Met His His Leu Ile Gln Pro
        675                 680                 685

Thr Met Glu Thr Thr Gln Pro Thr Gln Gln Gln Gln Gln Thr Ser Gln
    690                 695                 700

Gln Gln Gln Gln Pro Gln Gln Pro Gln Ala Thr Leu Thr Ser Pro His
705                 710                 715                 720

His Gln Gln Met Gln His Gln Ser Pro Ile His Gln Gln Gln Gln Ser
                725                 730                 735

Pro His His Gln Gln His Leu Pro Ser Tyr Asn Gln Ser Gln Gln Gln
            740                 745                 750

Phe Asp Pro Phe Ala Asn Ile Leu Gly Asp Asn Gln Pro Ala Ala Ser
        755                 760                 765

Gln Gln Thr Met Ser Pro Ala His Val Ser Ser Pro Val Pro Ala Gln
    770                 775                 780

Met Gln Gln Gln Gln His Gln Thr Gln Gln Gln Pro Ser Gln Gln Val
785                 790                 795                 800

Pro Gln Ser Gln Gln Gln Gln Val Ser Gln Pro Gln Gln Gln Thr Gln
                805                 810                 815

Gln Gln Gln Pro Ser Thr Pro Ser His His Leu Ser Ser Ile Leu Asn
            820                 825                 830
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Glu Thr Ala Asn Ser Asn Asp Ser Ser Thr Leu Ala Val Ala Ala Asn
        835                 840                 845

Asp Ser Asn Asn Ser Ser Ser Asn Ser Ser Thr Asn Ser Ile Val Asn
    850                 855                 860

Asn Gln Pro Thr Ser Val His Asp Ser Asn Ser Gln Ser Ser Ile Asn
865                 870                 875                 880

Ser Ser Ser Asn Asn Gln Gln Gln Leu Leu Met Asp Asn Thr Asn Ser
                885                 890                 895

His Gly Gly Asn Ser Glu Ser Ala Gln Asn Ala Gly Val Asp Val Gly
            900                 905                 910

Leu Phe Asp Asn Asn Ser Met Ser Ser Asn Ser Ala Ala Val Ala Ala
        915                 920                 925

Val Ala Ser Asn Ala Ala Ser Ala Ala Ala Ala Leu Leu Asp Ser Asn
    930                 935                 940

Ser Gln Ser Ser Asn Ala Glu Phe Glu Lys Asn Gln Ser Glu Gly Glu
945                 950                 955                 960

Gly Leu Gly Val Val Glu Gly Val Ile Ala Asn Glu Thr Asp Leu Pro
                965                 970                 975

Gln Asp Glu Asn Ser Val Ser Lys Thr Gln Asp Ile Thr Leu Ser Thr
            980                 985                 990

Glu Leu Pro Thr Ile Gln Asp Asp  Leu Gln Glu Lys Pro  Thr Ala Glu
        995                 1000                1005

Met Glu  Gln Thr Gln Leu Gly  Gln Ser Leu Gly Asp  Leu Ser Lys
    1010                1015                1020

Ser Leu  Leu Glu Glu Pro Lys  Thr Val Glu Glu Ser  Gly Glu Asp
    1025                1030                1035

Lys Ser  Gln Ser Ala Pro Gly  Val Ala Pro Pro Ala  Asp Pro Ile
    1040                1045                1050

Ile Pro  Val Thr Gln Pro Pro  Gln Gln Gln Met Pro  Pro Ile Gly
    1055                1060                1065

Met Pro  Met His Pro Ile Ala  Pro Gly Tyr Glu Ala  Gln Ala Gln
    1070                1075                1080

Gly Gln  Gly His Met Pro Pro  Met Met Pro Pro Tyr  Gly Gly Ala
    1085                1090                1095

Pro Gly  Met Tyr Pro Pro Tyr  Pro Met Leu His Gln  Gln Glu Ile
    1100                1105                1110

Ala Ala  Leu Gln Gln Gln Ile  Gln Glu Leu Tyr Cys  Met Pro Pro
    1115                1120                1125

Gly His  Glu Leu Gln His Gln  Asp Lys Leu Met Arg  Met Gln Glu
    1130                1135                1140

Arg Leu  Asn Leu Leu Thr Gln  His Glu Val Asn Asp  Gln Cys Ala
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1145 1150 1155

Gly Gly Pro Gln Cys Leu Leu Phe Gln Asn Val Pro Pro Met Tyr
1160 1165 1170

Gly Pro Pro Gly Asn Pro Leu Leu Asn Gln Gln Met Val Glu Ser
1175 1180 1185

Pro Gln Val Ser Ser Thr Thr Gly Arg Gly Arg Gly Lys Ser Ala
1190 1195 1200

Asn Lys Pro Arg Lys Pro Arg Ala Lys Lys Gly Glu Lys Ala Gln
1205 1210 1215

Val Gly Gln Gln Gln Asp Leu Met Asp Ile Ser Gly Asn Val Ala
1220 1225 1230

Met Gly Ala Ala Asn Ala Val Ser Ser Ile Pro Thr Thr Gln Leu
1235 1240 1245

Pro Val Ser Glu Asp Cys Val Thr Gln Gly Ala Gly Asp Thr Ser
1250 1255 1260

Val Val Gly Met Leu Glu Tyr Ser Glu Gly Met Gly Asp Leu Ser
1265 1270 1275

Gln Asp Val His Ser Ala Asn Glu Leu Asp Thr Ser Thr Asp Gly
1280 1285 1290

Ser Gly Lys Lys Lys Lys Pro Arg Lys Pro Arg Thr Pro Lys Asp
1295 1300 1305

Pro Asn Lys Pro Pro Arg Asp Arg Thr Pro Lys Ala Lys Lys Pro
1310 1315 1320

Lys Asp Pro Asn Asp Pro Asn Ser Thr Glu Thr Pro Ala Ala Val
1325 1330 1335

Lys Lys Arg Ala Gly Ala Ser Lys Arg Arg Lys Gln Tyr Gly Glu
1340 1345 1350

Asp Gly Ala Glu Gln Thr Gly Glu Gly Ser Glu Val Glu Asp Asn
1355 1360 1365

Lys Pro Leu Val Pro Lys Ala Gly Ser Ala Asp Gly Glu Ala Glu
1370 1375 1380

Thr Thr Ser Gly Gly Thr Gly Val Asp Gly Glu Ser Pro Asp Tyr
1385 1390 1395

Asp Asp Ile Pro Val Ser Lys Ile Pro Arg Gly Ser Asn Glu Asp
1400 1405 1410

Glu Lys Glu Ala Glu Ala Gly Asp Glu Thr Val Asp Ser Val Pro
1415 1420 1425

Asp Ser Ala Gly Asp Pro Ala Ser Thr Pro Ser Arg Arg Asp Arg
1430 1435 1440

Lys Arg Ser Thr Ala Arg Ser Arg Arg Asn Ala Asn Ser Glu Glu
1445 1450 1455

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Gly Gly  Ser Ala Arg Lys Asn  Arg Gly Ser Leu Ser  Ala Lys Ala
    1460                 1465                 1470

Leu Lys  Lys Arg Arg Asn Arg  Gly Arg Ile Val Pro  Glu Ser Asp
    1475                 1480                 1485

Gly Glu  Asp Asp Thr Leu Asp  Arg Thr Pro Pro Pro  Ser Pro Pro
    1490                 1495                 1500

Pro Asp  Ser Glu Met Asp Ser  Asn Lys Arg Arg Ser  Ser Arg Asn
    1505                 1510                 1515

Thr Gln  Arg Lys Lys Tyr Ile  Asp Asp Val Met Leu  Arg Phe Ser
    1520                 1525                 1530

Asp Asp  Glu Asn Ser Leu Leu  Val Ala Ser Pro Val  Lys Lys Asp
    1535                 1540                 1545

Lys Lys  Pro Ser Ala Asn Ala  Ser Asn Ser Asn Ala  Gly Ser Asp
    1550                 1555                 1560

Val Glu  Lys Thr Glu Pro Gln  Ser Gly Ala Glu Gly  Asp Ala Ala
    1565                 1570                 1575

Gln Glu  Val Gly Glu Glu Lys  Ser Asn Leu Pro Leu  Asp Glu Ser
    1580                 1585                 1590

Ser Gln  Leu Glu Ala Ser Ser  Ser Thr Ser Ala Val  Ala Glu Lys
    1595                 1600                 1605

Glu Arg  Gln Ile Ser Thr Asp  Ala Ala Asn Ala Ala  Met Ser Ser
    1610                 1615                 1620

Lys Pro  Asn Tyr Val Tyr Ile  Asn Thr Gly Asp Glu  Asp Ser Met
    1625                 1630                 1635

Val Val  Gln Leu Val Leu Ala  Met Arg Met Gly Lys  Arg Glu Leu
    1640                 1645                 1650

Ile Leu  Asp Lys Pro Lys Glu  Lys Ala Pro Glu Pro  Lys Gln Asp
    1655                 1660                 1665

Glu Glu  Lys Ser Glu Leu Asp  Glu Ala Thr Thr Asp  Lys Pro Glu
    1670                 1675                 1680

Gly Asp  Glu Lys Phe Lys Thr  Glu Gly Glu Ser Lys  Lys Asp Leu
    1685                 1690                 1695

Thr Asp  Ser Glu Glu Thr Lys  Leu Glu Ser Ser Ala  Met Glu Val
    1700                 1705                 1710

Asp Ser  Lys Glu Glu Ser Glu  Pro Asp Asp Ser Lys  Lys Ser Asp
    1715                 1720                 1725

Glu Asp  Asn Lys Asp Lys Asp  Lys Met Glu Val Asp  Asp Glu Val
    1730                 1735                 1740

Gly Lys  Ser Asp Lys Glu Ser  Lys Pro Glu Glu Gln  Ser Glu Thr
    1745                 1750                 1755
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Val Lys  Thr Glu Glu Asn Ser  Lys Ala Ile Glu Glu  Asp Lys Ser
    1760                 1765                 1770

Ser Thr  Val Leu Thr Ala Asp  His Ala Lys Glu Pro  Glu Thr Val
    1775                 1780                 1785

Leu Glu  Lys Met Glu Val Asp  Glu Lys Ala Asn Asp  Asp Gln Ser
    1790                 1795                 1800

Ala Val  Ser Lys Ala Glu Gly  Ser Asp Glu Lys Ser  Thr Asp Asp
    1805                 1810                 1815

Ser Asn  Pro Glu Glu Ala Thr  Thr Glu Lys Asn Lys  Glu Ser Leu
    1820                 1825                 1830

Glu Ile  Glu Gly Glu Lys Glu  Arg Val Lys Glu Gly  Glu Glu Ser
    1835                 1840                 1845

Val Lys  Lys Glu Asn Asp Glu  Lys Thr Glu Ala Asp  Met Glu Asn
    1850                 1855                 1860

Lys Pro  Glu Pro Val Phe Ile  Asp Val Glu Glu Tyr  Phe Val Lys
    1865                 1870                 1875

Tyr Arg  Asn Phe Ser Tyr Leu  His Cys Glu Trp Arg  Thr Glu Glu
    1880                 1885                 1890

Glu Leu  Leu Lys Gly Asp Arg  Arg Val Ala Ala Lys  Ile Arg Arg
    1895                 1900                 1905

Phe Gln  Gln Lys Gln Ser Gln  Gln Leu Asn Ile Phe  Glu Asn Ile
    1910                 1915                 1920

Glu Asp  Glu Pro Phe Asn Gln  Asp Phe Thr Glu Val  Asp Arg Val
    1925                 1930                 1935

Leu Asp  Met Ser Val His Thr  Asp Glu Thr Ser Gly  Glu Thr Thr
    1940                 1945                 1950

Lys His  Tyr Leu Val Lys Trp  Lys Ser Leu Pro Tyr  Glu Asp Cys
    1955                 1960                 1965

Thr Trp  Glu Leu Glu Glu Asp  Val Asp Asn Asp Lys  Ile Glu Gln
    1970                 1975                 1980

Tyr Leu  Arg Phe Asn Lys Ile  Pro Gln Arg Ser Glu  Trp Lys Ser
    1985                 1990                 1995

Lys Lys  Arg Pro His Pro Glu  Leu Trp Lys Lys Leu  Glu Lys Thr
    2000                 2005                 2010

Pro Val  Tyr Lys Gly Gly Asn  Ser Leu Arg Pro Tyr  Gln Leu Glu
    2015                 2020                 2025

Gly Leu  Asn Trp Leu Lys Phe  Ser Trp Tyr Asn Thr  His Asn Cys
    2030                 2035                 2040

Ile Leu  Ala Asp Glu Met Gly  Leu Gly Lys Thr Ile  Gln Ser Leu
    2045                 2050                 2055

Thr Phe  Val His Ser Val Tyr  Glu Tyr Gly Ile Arg  Gly Pro Phe
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2060 2065 2070

Leu Val Ile Ala Pro Leu Ser Thr Ile Pro Asn Trp Gln Arg Glu
2075 2080 2085

Phe Glu Gly Trp Thr Asp Met Asn Val Val Val Tyr His Gly Ser
2090 2095 2100

Val Thr Ser Lys Gln Met Ile Gln Asp Tyr Glu Tyr Tyr Tyr Lys
2105 2110 2115

Thr Glu Ser Gly Lys Val Leu Lys Glu Pro Ile Lys Phe Asn Val
2120 2125 2130

Leu Ile Thr Thr Phe Glu Met Ile Val Thr Asp Tyr Met Asp Leu
2135 2140 2145

Lys Ala Phe Asn Trp Arg Leu Cys Val Ile Asp Glu Ala His Arg
2150 2155 2160

Leu Lys Asn Arg Asn Cys Lys Leu Leu Glu Gly Leu Arg Gln Leu
2165 2170 2175

Asn Leu Glu His Arg Val Leu Leu Ser Gly Thr Pro Leu Gln Asn
2180 2185 2190

Asn Ile Ser Glu Leu Phe Ser Leu Leu Asn Phe Leu Glu Pro Ser
2195 2200 2205

Gln Phe Ser Ser Gln Glu Glu Phe Met Ser Glu Phe Gly Ser Leu
2210 2215 2220

Arg Thr Glu Glu Glu Ser Asp Gly Ala Leu Leu Gly Tyr Pro
2225 2230 2235

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<212> DNA
<213> Drosophila melanogaster

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ttggatgtaa aactaaatga aaatgtggaa aacgaagagc ttgttatatc cgaagggagt 180

caaccatcta aaagggcccg tctgggcgtg tgttcaacgt gcctgggttt attctccaaa 240

gactttcaga atgagctgct cagcagcatt ttggcatcgg atttcgcgaa atacgattgc 300

cagaaaatcg ttctggcgat ttgtctaccg atgtcgcttc agttgagaca gctggccatg 360

tggtttgcct tgcgaagaag atttggacca tctatagacg aaaacaatcc cccagacgtg 420

cctataaaag aggctgtcaa gctgatccta caccctataa tctgtgaaaa gctggccaag 480

ggttacgatg ccaacggtct gatgatcaat atagacctca cgcacagtct ggaaggcgaa 540

gaggtggaaa aactggtcaa attaaacaaa gaagcctttc ccgccaaggc ctcgcatcaa 600

aagcgcattg aaatttcgcg aggtttacta gagaaacagt atcaaccctc caaagttaag 660

gcggaaacct atgagaaata ttttcagata ccctgctcta acgtagagga atctataaaa 720

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accttcatgt cgagtggcag agaagatgtg gacgtccgat gcctggggaa aggaaggcct 960

tttgttctag aaattccaaa tgccaagttg gttgctctat aa 1002

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<211> 333
<212> PRT
<213> Drosophila melanogaster

<400> 8

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Glu Ile Cys Gln Leu Arg Tyr Leu Lys Ala Arg Gly Ala Glu Tyr Arg
20 25 30

Asn Ile Asn Glu Thr Leu Gln Lys Leu Asp Val Lys Leu Asn Glu Asn
35 40 45

Val Glu Asn Glu Glu Leu Val Ile Ser Glu Gly Ser Gln Pro Ser Lys
50 55 60

Arg Ala Arg Leu Gly Val Cys Ser Thr Cys Leu Gly Leu Phe Ser Lys
65 70 75 80

Asp Phe Gln Asn Glu Leu Leu Ser Ser Ile Leu Ala Ser Asp Phe Ala
85 90 95

Lys Tyr Asp Cys Gln Lys Ile Val Leu Ala Ile Cys Leu Pro Met Ser
100 105 110

Leu Gln Leu Arg Gln Leu Ala Met Trp Phe Ala Leu Arg Arg Arg Phe
115 120 125

Gly Pro Ser Ile Asp Glu Asn Asn Pro Pro Asp Val Pro Ile Lys Glu
130 135 140

Ala Val Lys Leu Ile Leu His Pro Ile Ile Cys Glu Lys Leu Ala Lys
145 150 155 160

Val Tyr Asp Ala Asn Gly Leu Met Ile Asn Ile Asp Leu Thr His Ser
165 170 175

Leu Glu Gly Glu Glu Val Glu Lys Leu Val Lys Leu Asn Lys Glu Ala
180 185 190

Phe Pro Ala Lys Ala Ser His Gln Lys Arg Ile Glu Ile Ser Arg Gly
195 200 205

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Leu Leu Glu Lys Gln Tyr Gln Pro Ser Lys Val Lys Ala Glu Thr Tyr
    210                 215                 220

Glu Lys Tyr Phe Gln Ile Pro Cys Ser Asn Val Glu Glu Ser Ile Lys
225                 230                 235                 240

Leu Thr Ser Ile Asp Leu Gln Gly Pro Leu Ile Cys Val Ala Gly Arg
                245                 250                 255

Tyr Arg Lys Leu Ser Arg Glu Leu Ser His Thr Pro Trp Ile Leu Asn
            260                 265                 270

Gly Gln Arg Leu Met Glu Asp Ser Ile Glu Glu Ile Ile Ile Arg His
        275                 280                 285

Val Gly Pro His Phe Thr Glu Lys Leu Gly Lys Ile Thr Phe Met Ser
    290                 295                 300

Ser Gly Arg Glu Asp Val Asp Val Arg Cys Leu Gly Lys Gly Arg Pro
305                 310                 315                 320

Phe Val Leu Glu Ile Pro Asn Ala Lys Arg Ser Cys Leu
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<211> 2208
<212> DNA
<213> Drosophila melanogaster

<400> 9

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gtgcagtgcg aaatagaaac aagaaaagca agcgaaaaat cacagaaatt cacaaaaaaa    180

aagcccaact acttccaaaa ttgggccgcc cggcgaagaa ccgcaaaagt ggccaaaatt    240

cggcgaaaac agcgcaagtg tgacaaagca ttcgtgccgc tgcagtcgtc ggcgaaacgg    300

gcgaaaacaa aagagaatag tgttgatagt aatacgagcg tatttagcag tagcagcagc    360

agcagcagtg gccgaagctt cggcagggga acggaacggt gggcggtggg tgcagaagcg    420

ggccggggaa cggccgagaa cgaaacacta gcagtagcag cagcagcagc gacaacaaca    480

aatgccggtc gctttatcac cgccgatcta atcaaaacag ttaacagcga caagcagcga    540

gacagagtag caaagggcca cagggacgcg aaaaaccccc tagatgccac caaacatttg    600

cgcctatcgg actgcttgcg taccgtgcaa aaacttgcta ttgaacttga gagcgccgac    660

gccggcagcg acgccagcgc ccaagccaac gctagcgccg acgccagcag cgccgtcatg    720

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tgcatctact tcggatgtcg gggggcccac atcacgagtc acctgcgatc caagaagcac    960
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cagaagagca tcggctgggt gccgtgggtt cccacaacca aggagaccaa tctgctgctg 1140

gccaatgcga ggcgtcggct ggtgaggccc aatcaaacga tcggactgag gggtctgctt 1200

aatctgggcg ccacttgctt catgaactgc atcgtccagg ctctggttca cacgcccctg 1260

ctcagcgatt actttatgtc agatcgtcac gactgcggca gcaagtcatc gcacaaatgt 1320

ctcgtttgtg aagtgtcacg tctcttccag gagttctatt ccggctcccg ttcgccgctg 1380

tcgctgcacc ggctactgca tttaatctgg aaccatgcga agcacttggc cggctacgag 1440

cagcaggatg cgcacgagtt cttcatcgcc actctggacg tgctgcatcg gcactgcgtg 1500

aaggcaaagg cggagcacga aagcaagagc aacagctctg gctcgggaag tggaaccaat 1560

tccagcaact cgagcagctc gcattgctac ggccagtgta attgcatcat tgaccagatc 1620

ttcacgggca tgctgcagag cgatgtggtg tgccaggcct gcaacggagt gtccaccacg 1680

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atgtcggaga agaagaacgc ctacggcgac ttccggttct ctctgtacgc cgtggtcaat 2040

catgtgggca ccatcgacac cggccactat acggcgtatg tgcggcacca gaaggacacg 2100

tgggtcaagt gcgatgatca tgtgataacg atggcatcgc tcaagcaggt gctggacagc 2160

gagggttatt tattgttcta ccataaaaat gtgctggaat acgagtaa 2208

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<211> 735
<212> PRT
<213> Drosophila melanogaster

<400> 10

Met Phe Gln Tyr Ser Tyr Ile Arg Lys Ile Pro Met Pro Thr Ser Glu
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Tyr Asp Phe Ala Thr Gly His Thr Asp Ser Cys Leu Leu Pro Thr His
20 25 30

Met Arg Ala Cys Val Cys Val Cys Val Gln Cys Glu Ile Glu Thr Arg
35 40 45

Lys Ala Ser Glu Lys Ser Gln Lys Phe Thr Lys Lys Lys Pro Asn Tyr

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    50                  55                  60

Phe Gln Asn Trp Ala Ala Arg Arg Arg Thr Ala Lys Val Ala Lys Ile
65                  70                  75                  80

Arg Arg Lys Gln Arg Lys Cys Asp Lys Ala Phe Val Pro Leu Gln Ser
                85                  90                  95

Ser Ala Lys Arg Ala Lys Thr Lys Glu Asn Ser Val Asp Ser Asn Thr
            100                 105                 110

Ser Val Phe Ser Ser Ser Ser Ser Ser Ser Ser Gly Arg Ser Phe Gly
        115                 120                 125

Arg Gly Thr Glu Arg Trp Ala Val Gly Ala Glu Ala Gly Arg Gly Thr
    130                 135                 140

Ala Glu Asn Glu Thr Leu Ala Val Ala Ala Ala Ala Ala Thr Thr Thr
145                 150                 155                 160

Asn Ala Gly Arg Phe Ile Thr Ala Asp Leu Ile Lys Thr Val Asn Ser
                165                 170                 175

Asp Lys Gln Arg Asp Arg Val Ala Lys Gly His Arg Asp Ala Lys Asn
            180                 185                 190

Pro Leu Asp Ala Thr Lys His Leu Arg Leu Ser Asp Cys Leu Arg Thr
        195                 200                 205

Val Gln Lys Leu Ala Ile Glu Leu Glu Ser Ala Asp Ala Gly Ser Asp
    210                 215                 220

Ala Ser Ala Gln Ala Asn Ala Ser Ala Asp Ala Ser Ser Ala Val Met
225                 230                 235                 240

Ser Glu Thr Gly Cys Arg His Tyr Gln Ser Tyr Val Lys Glu His Ser
                245                 250                 255

Tyr Asp Thr Phe Arg Val Ile Asp Ala Tyr Phe Ala Ala Cys Val Asn
            260                 265                 270

Arg Asp Ala Arg Glu Arg Lys Ala Ile His Cys Asn Cys Phe Glu Cys
        275                 280                 285

Gly Ser Tyr Gly Ile Gln Leu Tyr Ala Cys Leu His Cys Ile Tyr Phe
    290                 295                 300

Gly Cys Arg Gly Ala His Ile Thr Ser His Leu Arg Ser Lys Lys His
305                 310                 315                 320

Asn Val Ala Leu Glu Leu Ser His Gly Thr Leu Tyr Cys Tyr Ala Cys
                325                 330                 335

Arg Asp Phe Ile Tyr Asp Ala Arg Ser Arg Glu Tyr Ala Leu Ile Asn
            340                 345                 350

Arg Lys Leu Glu Ala Lys Asp Leu Gln Lys Ser Ile Gly Trp Val Pro
        355                 360                 365

Trp Val Pro Thr Thr Lys Glu Thr Asn Leu Leu Leu Ala Asn Ala Arg
    370                 375                 380
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Arg Arg Leu Val Arg Pro Asn Gln Thr Ile Gly Leu Arg Gly Leu Leu
385                 390                 395                 400

Asn Leu Gly Ala Thr Cys Phe Met Asn Cys Ile Val Gln Ala Leu Val
                405                 410                 415

His Thr Pro Leu Leu Ser Asp Tyr Phe Met Ser Asp Arg His Asp Cys
            420                 425                 430

Gly Ser Lys Ser Ser His Lys Cys Leu Val Cys Glu Val Ser Arg Leu
        435                 440                 445

Phe Gln Glu Phe Tyr Ser Gly Ser Arg Ser Pro Leu Ser Leu His Arg
    450                 455                 460

Leu Leu His Leu Ile Trp Asn His Ala Lys His Leu Ala Gly Tyr Glu
465                 470                 475                 480

Gln Gln Asp Ala His Glu Phe Phe Ile Ala Thr Leu Asp Val Leu His
                485                 490                 495

Arg His Cys Val Lys Ala Lys Ala Glu His Glu Ser Lys Ser Asn Ser
            500                 505                 510

Ser Gly Ser Gly Ser Gly Thr Asn Ser Ser Asn Ser Ser Ser Ser His
        515                 520                 525

Cys Tyr Gly Gln Cys Asn Cys Ile Ile Asp Gln Ile Phe Thr Gly Met
    530                 535                 540

Leu Gln Ser Asp Val Val Cys Gln Ala Cys Asn Gly Val Ser Thr Thr
545                 550                 555                 560

Tyr Asp Pro Phe Trp Asp Ile Ser Leu Asp Leu Gly Glu Thr Thr Thr
                565                 570                 575

His Gly Gly Val Thr Pro Lys Thr Leu Ile Asp Cys Leu Glu Arg Tyr
            580                 585                 590

Thr Arg Ala Glu His Leu Gly Ser Ala Ala Lys Ile Lys Cys Ser Thr
        595                 600                 605

Cys Lys Ser Tyr Gln Glu Ser Thr Lys Gln Phe Ser Leu Arg Thr Leu
    610                 615                 620

Pro Ser Val Val Ser Phe His Leu Lys Arg Phe Glu His Ser Ala Leu
625                 630                 635                 640

Ile Asp Arg Lys Ile Ser Ser Phe Ile Gln Phe Pro Val Glu Phe Asp
                645                 650                 655

Met Thr Pro Phe Met Ser Glu Lys Lys Asn Ala Tyr Gly Asp Phe Arg
            660                 665                 670

Phe Ser Leu Tyr Ala Val Val Asn His Val Gly Thr Ile Asp Thr Gly
        675                 680                 685

His Tyr Thr Ala Tyr Val Arg His Gln Lys Asp Thr Trp Val Lys Cys
    690                 695                 700
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Asp Asp His Val Ile Thr Met Ala Ser Leu Lys Gln Val Leu Asp Ser
705 710 715 720

Glu Gly Tyr Leu Leu Phe Tyr His Lys Asn Val Leu Glu Tyr Glu
725 730 735

<210> 11
<211> 1602
<212> DNA
<213> Drosophila melanogaster

<400> 11
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gagaacagtg aggacaatga aaacagcgcg tccggcaccg ttagggaaca gcgtgacgag 120

gcggcgggcc gcaccgttct ccagtgggcg tggcatgtgg tcaaatccac atccgtggag 180

cccacaatgt tcctgtacat gttcgccttc atgatcacct cggtggtgga gcagaacttc 240

ttcctctaca agtcctgtcg ggttaacaga aatttcacgg aggagatctg caggaatctc 300

aacaagccgg agaacgagga gttccgaacg aaggcaatgt tgaccaatgc ctggttcctt 360

cagtgggaga acatttctgc ccacgttttc cccattattc tggccctttt tctgggctcc 420

ttctcggatc ggcggggccg aaagttgccc ctgctcatgg gactagtggg aaagtttttc 480

tactccacga tgatagtggt caacgctagg atgaccacgt ggccggtgca aaacatcatc 540

tactcggcga cgttgccatc ggcgttgacc ggtgcggatg tggccatttt cgcctcctgc 600

ttcgcctaca tctcggacat ttcctcgctg cagcagcgca ccattcgggt gaccattctg 660

gacgtgatct acctcagtgc catgcccatg ggcgtggccc tgggctcgca tctcttttac 720

aacgtgttca atcagtccta tgcggacatg ttcaccgtaa acgcttcact acttgccctc 780

gccatcatct acaccctgtg cgccctgaag tggcaaacga cgccgagaca gcgatcgttg 840

agggaactcg gatgctgtgg cttttggggc gacttctttg ataagcagca tgtgaaggac 900

tcgttggcgg tgttggtgaa gccgcgaaag ggtcatcgtc gcagctttct cattatcctt 960

ctggtcagca tggcactgta caccttccag cgtgacgagg ggcagtatct ctacatgtac 1020

accctgggca aatttgactg ggatgtgagt gcgtacagca acttcaagac attcaagtca 1080

tcggcctacg tgattgccat gctattggct gtgccgctga tgaacaagat ccttggatgg 1140

agggatacga caatcatttt cattggcacc tgggcccatt cgatagcccg cttgttcttc 1200

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attgtgggtc ccatgatccg ggccatgacc tcgaaaatag tgcccacatc agagcgcgga 1320

aaggtatttg cactgctatc agtttgcgat aatgcggtgc ccttcatcag cggtgtgtgc 1380

tattcgcaac tttataggcg cactcagaat acgaatcacg gaggaaatgt cttcatccta 1440

accattgcca cccaaatcgc tgtctttgtg atgatacttt gcttacacat tgttttgggc 1500

aaaaattcac tggctgttcc ggaagttcct gagaaggaga gcggacttat ttcccaaacg 1560

gaagctgtcc tggaggcgga aattgaggag cacaagaact ag 1602

<210> 12
<211> 533
<212> PRT
<213> Drosophila melanogaster

<400> 12

Met Ser Val Thr Gly Ala His Ser Glu Asn Ala Ala Gln Arg Arg Asn
1 5 10 15

Ser Arg Ser Ser Glu Asn Ser Glu Asp Asn Glu Asn Ser Ala Ser Gly
20 25 30

Thr Val Arg Glu Gln Arg Asp Glu Ala Ala Gly Arg Thr Val Leu Gln
35 40 45

Trp Ala Trp His Val Val Lys Ser Thr Ser Val Glu Pro Thr Met Phe
50 55 60

Leu Tyr Met Phe Ala Phe Met Ile Thr Ser Val Val Glu Gln Asn Phe
65 70 75 80

Phe Leu Tyr Lys Ser Cys Arg Val Asn Arg Asn Phe Thr Glu Glu Ile
85 90 95

Cys Arg Asn Leu Asn Lys Pro Glu Asn Glu Glu Phe Arg Thr Lys Ala
100 105 110

Met Leu Thr Asn Ala Trp Phe Leu Gln Trp Glu Asn Ile Ser Ala His
115 120 125

Val Phe Pro Ile Ile Leu Ala Leu Phe Leu Gly Ser Phe Ser Asp Arg
130 135 140

Arg Gly Arg Lys Leu Pro Leu Leu Met Gly Leu Val Gly Lys Phe Phe
145 150 155 160

Tyr Ser Thr Met Ile Val Val Asn Ala Arg Met Thr Thr Trp Pro Val
165 170 175

Gln Asn Ile Ile Tyr Ser Ala Thr Leu Pro Ser Ala Leu Thr Gly Ala
180 185 190

Asp Val Ala Ile Phe Ala Ser Cys Phe Ala Tyr Ile Ser Asp Ile Ser
195 200 205

Ser Leu Gln Gln Arg Thr Ile Arg Val Thr Ile Leu Asp Val Ile Tyr
210 215 220

Leu Ser Ala Met Pro Met Gly Val Ala Leu Gly Ser His Leu Phe Tyr
225 230 235 240

Asn Val Phe Asn Gln Ser Tyr Ala Asp Met Phe Thr Val Asn Ala Ser
245 250 255

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Leu Leu Ala Leu Ala Ile Ile Tyr Thr Leu Cys Ala Leu Lys Trp Gln
            260                 265                 270

Thr Thr Pro Arg Gln Arg Ser Leu Arg Glu Leu Gly Cys Cys Gly Phe
        275                 280                 285

Trp Gly Asp Phe Phe Asp Lys Gln His Val Lys Asp Ser Leu Ala Val
    290                 295                 300

Leu Val Lys Pro Arg Lys Gly His Arg Arg Ser Phe Leu Ile Ile Leu
305                 310                 315                 320

Leu Val Ser Met Ala Leu Tyr Thr Phe Gln Arg Asp Glu Gly Gln Tyr
                325                 330                 335

Leu Tyr Met Tyr Thr Leu Gly Lys Phe Asp Trp Asp Val Ser Ala Tyr
            340                 345                 350

Ser Asn Phe Lys Thr Phe Lys Ser Ser Ala Tyr Val Ile Ala Met Leu
        355                 360                 365

Leu Ala Val Pro Leu Met Asn Lys Ile Leu Gly Trp Arg Asp Thr Thr
    370                 375                 380

Ile Ile Phe Ile Gly Thr Trp Ala His Ser Ile Ala Arg Leu Phe Phe
385                 390                 395                 400

Tyr Phe Ala Thr Asn Thr Asp Leu Leu Tyr Ala Gly Ala Val Val Cys
                405                 410                 415

Ser Leu Gly Pro Ile Val Gly Pro Met Ile Arg Ala Met Thr Ser Lys
            420                 425                 430

Ile Val Pro Thr Ser Glu Arg Gly Lys Val Phe Ala Leu Leu Ser Val
        435                 440                 445

Cys Asp Asn Ala Val Pro Phe Ile Ser Gly Val Cys Tyr Ser Gln Leu
    450                 455                 460

Tyr Arg Arg Thr Gln Asn Thr Asn His Gly Gly Asn Val Phe Ile Leu
465                 470                 475                 480

Thr Ile Ala Thr Gln Ile Ala Val Phe Val Met Ile Leu Cys Leu His
                485                 490                 495

Ile Val Leu Gly Lys Asn Ser Leu Ala Val Pro Glu Val Pro Glu Lys
            500                 505                 510

Glu Ser Gly Leu Ile Ser Gln Thr Glu Ala Val Leu Glu Ala Glu Ile
        515                 520                 525

Glu Glu His Lys Asn
    530
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<210> 13
<211> 3261
<212> DNA
<213> Drosophila melanogaster

<400> 13
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tttacgcaac aatttacaga gaatgatttc gagggacatc gggcccacac cgtttatgtg 120

ttcatcttca tctacaaggc tattgagaac gtgatggtca ttggaaagaa cttcccggtc 1920

aatcagggca tatacgactg tgtctgtaca ccgccaattg ggagcaatgc cagtgtgatc 1980

gattatgcca agtacaattg ggattcttgt gagtcctaca atggcacctt ggttggtgga 2040

gattgcggaa cgccgcccac cgaaaacgtt ttcctcatgt cggtggtcct ctgcgccggc 2100

accttcctca tctccaccgt gctgaaggag ttcaaaaacg ccctattctt cccatcgatt 2160

gtccgccagt atatcagcga tttctccgtt ctcatcgcga ttttcgccat gagtttcttc 2220

gactattcgc tgggagttcc cacccagaaa ctggaggtac ccaacgagct gaagcccacg 2280

ctaagcacca gaggctggct catcccgccg ttcgtcgaga agaatccctg gtggtcggcg 2340

atcattgccg tattccctgc ccttctcgga accatcctga tcttcatgga ccagcagatc 2400

acggccgtta ttgtgaaccg aaaggagaac aaactgaaga agggatgtgg ctaccatctg 2460

gatctgttca ttctctccat tctgattgcc atctgcagca tgatgggtct gccttggttc 2520

gtggccgcca ccgtgctgag catcaaccac gtgaactcgc tgaaactgga gtcggagtgc 2580

tcggcccctg gtgagaagcc acagttcctg ggagtgcgcg agcagcgggt gacccacatc 2640

ttgatcttcc tgaccatcgg cgtctccgtg ctgttgaccc cgctgctcgg taacattcct 2700

atgccggttc ttttcggtgt ctttctgtat atgggcgtgg cctcactcaa gggcttacag 2760

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ctgcgccagg ttcccattaa acgcgtccac ctgttcacca tgatccagct ggcctgcctc 2880

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gtggtgatga ttggcatcag aaaggccctg gatctggtgt tcactcggcg cgagctgaag 3000

atcctggacg acataatgcc ggagatgacg aagcgtgcgg cggcggatga tctgcataaa 3060

ctggacgctg aggtgggctt attggcgcgc attttccccc ggggaaaagg cagccggagc 3120

agggtggtga ccaagccgcc gggccttgat gatggaatcg ttgggtctgg tggtgccgtt 3180

ggcgctggac tcatcacttg caccacctca aatgcaaatg agaaggagtt cgaggcacag 3240

agtagtctgc tcaaaaagta g 3261

<210> 14
<211> 1086
<212> PRT
<213> Drosophila melanogaster

<400> 14

Met Asn Ser Ser Ser Gly Asp Asp Glu Ala Pro Lys Asp Pro Arg Thr
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Gly Gly Glu Asp Phe Thr Gln Gln Phe Thr Glu Asn Asp Phe Glu Gly
20 25 30

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His Arg Ala His Thr Val Tyr Val Gly Val His Val Pro Gly Gly Arg
        35                  40                  45

Arg His Ser Gln Arg Arg Arg Lys His His His Ser Gly Pro Gly Gly
    50                  55                  60

Gly Gly Gly Gly Gly Gly Gly Gly Gly Ser Ile Gly Gly Ser Gly Ser
65                  70                  75                  80

Val Gly Gly Gly Ala Gly Lys Asp Asn Val Ser Glu Lys Gln Gln Glu
                85                  90                  95

Val Glu Arg Pro Val Thr Pro Pro Ala Gln Arg Val Gln Phe Ile Leu
            100                 105                 110

Gly Glu Asp Val Asp Asp Gly Thr His Val Ser His Pro Leu Phe Ser
        115                 120                 125

Glu Met Gly Met Leu Val Lys Glu Gly Asp Glu Ile Glu Trp Lys Glu
    130                 135                 140

Thr Ala Arg Trp Ile Lys Phe Glu Glu Asp Val Glu Glu Gly Gly Asn
145                 150                 155                 160

Arg Trp Ser Lys Pro His Val Ala Thr Leu Ser Leu His Ser Leu Phe
                165                 170                 175

Glu Leu Arg Arg Leu Leu Val Asn Gly Ser Val Met Leu Asp Met Glu
            180                 185                 190

Ala Gln Asn Leu Glu Val Met Ala Asp Leu Val Cys Asp His Met Val
        195                 200                 205

Ser Ala Gly Thr Leu Pro Pro Gly Val Lys Asp Lys Val Lys Asp Ala
    210                 215                 220

Leu Leu Arg Arg His Arg His Gln His Glu Tyr Ala Lys Lys Thr Arg
225                 230                 235                 240

Leu Pro Ile Ile Arg Ser Leu Ala Asp Met Arg Asn His Ser Ser Ser
                245                 250                 255

Lys Lys Lys Lys Ser Asn Ser Lys His Ser Arg Pro Ala Gln Asn Leu
            260                 265                 270

Ser Ser Ile Thr Glu Asp Met Val Lys Ser Pro Ser Asn Gln Ser Met
        275                 280                 285

Ala Arg Pro Gly Ser Gly Thr Glu Leu Ser Glu Gln Gln His Lys Gly
    290                 295                 300

Asn Thr His Phe Met Arg Lys Ile Pro Pro Gly Ala Glu Ala Ser Asn
305                 310                 315                 320

Ile Leu Val Gly Glu Val Asp Phe Leu Glu Arg Thr Leu Ser Cys Phe
                325                 330                 335

Ile Arg Leu Ser Gln Ala Val Val Leu Gly Asp Leu Thr Glu Val Pro
            340                 345                 350
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Val Pro Thr Arg Phe Val Phe Ile Leu Leu Gly Pro Pro Gly Ser Gln
355 360 365

Ser Asn Phe His Glu Ile Gly Arg Ala Met Ala Thr Leu Met Ser Asp
370 375 380

Glu Ile Phe His Glu Val Ala Tyr Arg Ala Arg Lys Arg Asp His Leu
385 390 395 400

Leu Ser Gly Val Asp Glu Phe Leu Asp Ala Val Thr Val Leu Pro Pro
405 410 415

Gly Glu Trp Asp Pro Thr Ile Arg Ile Glu Pro Pro Ala Ala Ile Pro
420 425 430

Ser Gln Glu Val Arg Lys Arg Pro Pro Glu Leu Pro Lys Glu Glu Val
435 440 445

Asp Glu Glu Glu Glu Glu Ala Arg Leu Arg Glu Glu Asn Gly Leu Ser
450 455 460

Arg Thr Gly Arg Leu Phe Gly Gly Leu Ile Asn Asp Ile Lys Arg Lys
465 470 475 480

Ala Pro Trp Tyr Ile Ser Asp Tyr Lys Asp Ala Leu Ser Met Gln Cys
485 490 495

Val Ala Ser Trp Ile Phe Leu Tyr Phe Ala Cys Leu Ser Pro Ile Ile
500 505 510

Thr Phe Gly Gly Leu Leu Ala Glu Ala Thr Gly Lys His Met Ala Ala
515 520 525

Met Glu Ser Leu Val Ser Gly Phe Val Cys Gly Met Gly Tyr Gly Phe
530 535 540

Phe Ser Gly Gln Pro Leu Thr Ile Leu Gly Ser Thr Gly Pro Val Leu
545 550 555 560

Val Phe Glu Ser Ile Ile Tyr Glu Phe Cys Leu Lys Met Gly Trp Asp
565 570 575

Tyr Met Thr Phe Arg Phe Trp Ile Gly Met Trp Val Ala Gly Ile Cys
580 585 590

Ile Val Leu Thr Ala Ile Asp Ala Ser Ala Leu Val Cys Tyr Ile Thr
595 600 605

Arg Phe Thr Glu Glu Asn Phe Ala Thr Leu Ile Ala Phe Ile Phe Ile
610 615 620

Tyr Lys Ala Ile Glu Asn Val Met Val Ile Gly Lys Asn Phe Pro Val
625 630 635 640

Asn Gln Gly Ile Tyr Asp Cys Val Cys Thr Pro Pro Ile Gly Ser Asn
645 650 655

Ala Ser Val Ile Asp Tyr Ala Lys Tyr Asn Trp Asp Ser Cys Glu Ser
660 665 670

Tyr Asn Gly Thr Leu Val Gly Gly Asp Cys Gly Thr Pro Pro Thr Glu

675 680 685

Asn Val Phe Leu Met Ser Val Val Leu Cys Ala Gly Thr Phe Leu Ile
690 695 700

Ser Thr Val Leu Lys Glu Phe Lys Asn Ala Leu Phe Phe Pro Ser Ile
705 710 715 720

Val Arg Gln Tyr Ile Ser Asp Phe Ser Val Leu Ile Ala Ile Phe Ala
725 730 735

Met Ser Phe Phe Asp Tyr Ser Leu Gly Val Pro Thr Gln Lys Leu Glu
740 745 750

Val Pro Asn Glu Leu Lys Pro Thr Leu Ser Thr Arg Gly Trp Leu Ile
755 760 765

Pro Pro Phe Val Glu Lys Asn Pro Trp Trp Ser Ala Ile Ile Ala Val
770 775 780

Phe Pro Ala Leu Leu Gly Thr Ile Leu Ile Phe Met Asp Gln Gln Ile
785 790 795 800

Thr Ala Val Ile Val Asn Arg Lys Glu Asn Lys Leu Lys Lys Gly Cys
805 810 815

Gly Tyr His Leu Asp Leu Phe Ile Leu Ser Ile Leu Ile Ala Ile Cys
820 825 830

Ser Met Met Gly Leu Pro Trp Phe Val Ala Ala Thr Val Leu Ser Ile
835 840 845

Asn His Val Asn Ser Leu Lys Leu Glu Ser Glu Cys Ser Ala Pro Gly
850 855 860

Glu Lys Pro Gln Phe Leu Gly Val Arg Glu Gln Arg Val Thr His Ile
865 870 875 880

Leu Ile Phe Leu Thr Ile Gly Val Ser Val Leu Leu Thr Pro Leu Leu
885 890 895

Gly Asn Ile Pro Met Pro Val Leu Phe Gly Val Phe Leu Tyr Met Gly
900 905 910

Val Ala Ser Leu Lys Gly Leu Gln Phe Phe Asp Arg Ile Leu Ile Met
915 920 925

Phe Met Pro Ala Lys Tyr Gln Pro Asp Tyr Met Phe Leu Arg Gln Val
930 935 940

Pro Ile Lys Arg Val His Leu Phe Thr Met Ile Gln Leu Ala Cys Leu
945 950 955 960

Ile Ile Leu Trp Leu Ile Lys Ser Phe Ser Gln Thr Ser Ile Leu Phe
965 970 975

Pro Leu Met Leu Val Val Met Ile Gly Ile Arg Lys Ala Leu Asp Leu
980 985 990

Val Phe Thr Arg Arg Glu Leu Lys Ile Leu Asp Asp Ile Met Pro Glu
995 1000 1005

Met Thr Lys Arg Ala Ala Ala Asp Asp Leu His Lys Leu Asp Ala
1010 1015 1020

Glu Val Gly Leu Leu Ala Arg Ile Phe Pro Trp Gly Lys Gly Ser
1025 1030 1035

Arg Ser Arg Val Val Thr Lys Pro Pro Gly Leu Asp Asp Gly Ile
1040 1045 1050

Val Gly Ser Gly Gly Ala Val Gly Ala Gly Leu Ile Thr Cys Thr
1055 1060 1065

Thr Ser Asn Ala Asn Glu Lys Glu Phe Glu Ala Gln Ser Ser Leu
1070 1075 1080

Leu Lys Lys
1085

<210> 15
<211> 1653
<212> DNA
<213> Drosophila melanogaster

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ccaaatcaag gggtccgtct ccagctgggc gcctggtggc aggtaaccat cggccgtcgc 120

attggcctct acagattctg tggcgacatc ggacgcggca atttctcgaa agtgaagctc 180

gctgtccacc aactgacgcg tgacaaagtg gccattaagg tggtggacct ggatcgggcc 240

ggactggatg ccaaggcact gcgaatgctg tccagcgaga tagccactct cgagtgtgtg 300

catcatccga atatactgag gcttttcgag gtggtcgaaa ctctgggccg cgtttacctg 360

gtcactgagt ggattcgcgg tggcgagcta tacaaccaca tcacccaagg cggtccgctg 420

cgggagattc atgcggcccc gttgctgaaa caactcctcc tggcagtcaa acatatgcac 480

agtctgggct acgtgcatcg ggacataaag gcggaaaatg tcctgctcct ctccgaggat 540

cgcctcaagc tggccgactt cggtttcagt acccaactca tcaatggtac gggtgccaat 600

caaaagctcg acacgttctg cggatcccct ccgtatgcgg cgcccgagct cttctccgat 660

gaccactaca taggggcgcc cgtggatgtt tgggccctgg gcatcctgct ctacttcatg 720

gtggtcggaa acatgccctt ccgggcacca acgattcccg gcctgaaagc agccatcctg 780

aagggtgact atctgctgcc cggccagctc agcttgccct gcataagact tatacaacgc 840

atcttgattc atatacccgc ccagcggcca accatcgacg acatgctgaa cagccagttc 900

gtgacctgtc ccaagctcag tgccgatctg atgcagtggg agatcaacca gcacaccaag 960

ccggtcaaga ggtccatctt ctgggtgcgc agcaagtcgc atcggctgcg gaagtccgcc 1020

tcactacggg atcgatacgc ggaggtggtc aagaagccgg ccattagcat gaacaccagg 1080

cagcaggacg agatgtttgt gcagaacttc ctgcaaccga tcgagatggg acacgaactg 1140

ttggtcccgg tgtcaagtca gctgaaggag ccacagtcca ccgagcaggc gaagcgtcca 1200

accagaaggt acatgttctg cggcagcctg aagaagaagg tcacgcccat ggaaacggaa 1260

ccggagaagc agctggccaa cggtggacag tcaatcggtt cggccaagat caatccgtgg 1320

aatgtggagg tggccgagga ttgccccctg ttcaagaact acgacgcgga gacgggcagc 1380

tgcgtcatgc tgcccacgaa caccgaggat ctgagccagc taggtgccct ggagttcgag 1440

gcacgccaga tcctggccga gctgggcctc acctccgaga tgctgatcaa cgccaggcag 1500

agcgggccgc gctccgacat cattggcgcc tacaggatcg tggtcaatcg gttgcagaag 1560

cagtcctggc tggcacgaaa gcacgtggag atggcactgc acagcgagcc caaggtggag 1620

aagcggattg agaggtcgtg ctgcatactc taa 1653

<210> 16
<211> 550
<212> PRT
<213> Drosophila melanogaster

<400> 16

Met Arg Ser Ala Leu Arg Pro Arg Gly Glu Cys Lys Leu Lys Cys Leu
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Trp Arg Arg Tyr Pro Asn Gln Gly Val Arg Leu Gln Leu Gly Ala Trp
20 25 30

Trp Gln Val Thr Ile Gly Arg Arg Ile Gly Leu Tyr Arg Phe Cys Gly
35 40 45

Asp Ile Gly Arg Gly Asn Phe Ser Lys Val Lys Leu Ala Val His Gln
50 55 60

Leu Thr Arg Asp Lys Val Ala Ile Lys Val Val Asp Leu Asp Arg Ala
65 70 75 80

Gly Leu Asp Ala Lys Ala Leu Arg Met Leu Ser Ser Glu Ile Ala Thr
85 90 95

Leu Glu Cys Val His His Pro Asn Ile Leu Arg Leu Phe Glu Val Val
100 105 110

Glu Thr Leu Gly Arg Val Tyr Leu Val Thr Glu Trp Ile Arg Gly Gly
115 120 125

Glu Leu Tyr Asn His Ile Thr Gln Gly Gly Pro Leu Arg Glu Ile His
130 135 140

Ala Ala Pro Leu Leu Lys Gln Leu Leu Leu Ala Val Lys His Met His
145 150 155 160

Ser Leu Gly Tyr Val His Arg Asp Ile Lys Ala Glu Asn Val Leu Leu
165 170 175

Leu Ser Glu Asp Arg Leu Lys Leu Ala Asp Phe Gly Phe Ser Thr Gln
180 185 190

Leu Ile Asn Gly Thr Gly Ala Asn Gln Lys Leu Asp Thr Phe Cys Gly
195 200 205

Ser Pro Pro Tyr Ala Ala Pro Glu Leu Phe Ser Asp Asp His Tyr Ile
210 215 220

Gly Ala Pro Val Asp Val Trp Ala Leu Gly Ile Leu Leu Tyr Phe Met
225 230 235 240

Val Val Gly Asn Met Pro Phe Arg Ala Pro Thr Ile Pro Gly Leu Lys
245 250 255

Ala Ala Ile Leu Lys Gly Asp Tyr Leu Leu Pro Gly Gln Leu Ser Leu
260 265 270

Pro Cys Ile Arg Leu Ile Gln Arg Ile Leu Ile His Ile Pro Ala Gln
275 280 285

Arg Pro Thr Ile Asp Asp Met Leu Asn Ser Gln Phe Val Thr Cys Pro
290 295 300

Lys Leu Ser Ala Asp Leu Met Gln Trp Glu Ile Asn Gln His Thr Lys
305 310 315 320

Pro Val Lys Arg Ser Ile Phe Trp Val Arg Ser Lys Ser His Arg Leu
325 330 335

Arg Lys Ser Ala Ser Leu Arg Asp Arg Tyr Ala Glu Val Val Lys Lys
340 345 350

Pro Ala Ile Ser Met Asn Thr Arg Gln Gln Asp Glu Met Phe Val Gln
355 360 365

Asn Phe Leu Gln Pro Ile Glu Met Gly His Glu Leu Leu Val Pro Val
370 375 380

Ser Ser Gln Leu Lys Glu Pro Gln Ser Thr Glu Gln Ala Lys Arg Pro
385 390 395 400

Thr Arg Arg Tyr Met Phe Cys Gly Ser Leu Lys Lys Lys Val Thr Pro
405 410 415

Met Glu Thr Glu Pro Glu Lys Gln Leu Ala Asn Gly Gly Gln Ser Ile
420 425 430

Gly Ser Ala Lys Ile Asn Pro Trp Asn Val Glu Val Ala Glu Asp Cys
435 440 445

Pro Leu Phe Lys Asn Tyr Asp Ala Glu Thr Gly Ser Cys Val Met Leu
450 455 460

Pro Thr Asn Thr Glu Asp Leu Ser Gln Leu Gly Ala Leu Glu Phe Glu
465 470 475 480

Ala Arg Gln Ile Leu Ala Glu Leu Gly Leu Thr Ser Glu Met Leu Ile
485 490 495

Asn Ala Arg Gln Ser Gly Pro Arg Ser Asp Ile Ile Gly Ala Tyr Arg

500 505 510

Ile Val Val Asn Arg Leu Gln Lys Gln Ser Trp Leu Ala Arg Lys His
515 520 525

Val Glu Met Ala Leu His Ser Glu Pro Lys Val Glu Lys Arg Ile Glu
530 535 540

Arg Ser Cys Cys Ile Leu
545 550

<210> 17
<211> 510
<212> DNA
<213> Drosophila melanogaster

<400> 17
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atcgcctcca agtgcggcct gaccaagaac aactacgaga agctgacgga tctaaaggag 180

aagtacggcg agcgcggcct ggtgatcctc aacttcccgt gcaatcagtt tgggtcccag 240

atgccggagg ccgatggaga ggccatggtg tgccacctgc gcgactccaa ggctgacatc 300

ggcgaggtgt tcgccaaggt cgatgtgaat ggagacaatg cggcgccgct gtacaaatac 360

ctaaaggcca agcagaccgg caccctgggc agcggaatca agtggaactt caccaagttt 420

ctggtgaaca aggagggcgt gcccatcaac cgatatgccc cgaccaccga tcccatggac 480

atcgccaagg acattgaaaa gctgctgtag 510

<210> 18
<211> 169
<212> PRT
<213> Drosophila melanogaster

<400> 18

Met Ser Ala Asn Gly Asp Tyr Lys Asn Ala Ala Ser Ile Tyr Glu Phe
1 5 10 15

Thr Val Lys Asp Thr His Gly Asn Asp Val Ser Leu Glu Lys Tyr Lys
20 25 30

Gly Lys Val Val Leu Val Val Asn Ile Ala Ser Lys Cys Gly Leu Thr
35 40 45

Lys Asn Asn Tyr Glu Lys Leu Thr Asp Leu Lys Glu Lys Tyr Gly Glu
50 55 60

Arg Gly Leu Val Ile Leu Asn Phe Pro Cys Asn Gln Phe Gly Ser Gln
65 70 75 80

Met Pro Glu Ala Asp Gly Glu Ala Met Val Cys His Leu Arg Asp Ser
85 90 95

Lys Ala Asp Ile Gly Glu Val Phe Ala Lys Val Asp Val Asn Gly Asp
100 105 110

Asn Ala Ala Pro Leu Tyr Lys Tyr Leu Lys Ala Lys Gln Thr Gly Thr
115 120 125

Leu Gly Ser Gly Ile Lys Trp Asn Phe Thr Lys Phe Leu Val Asn Lys
130 135 140

Glu Gly Val Pro Ile Asn Arg Tyr Ala Pro Thr Thr Asp Pro Met Asp
145 150 155 160

Ile Ala Lys Asp Ile Glu Lys Leu Leu
165

<210> 19
<211> 4491
<212> DNA
<213> Drosophila melanogaster

<400> 19
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ggcggggcat ccgtcgcata cgaatctcat catgagatca ccgatttgta a 4491

<210> 20
<211> 1496
<212> PRT
<213> Drosophila melanogaster

<400> 20

Met Glu Ile Phe Gln Ser Gln His Arg Gln Glu Ser Gln Ser Pro Asp
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Tyr His His Arg Tyr Ala Ser Asn Gly Lys Leu Pro Arg Ala Ala Ala

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Leu Ser Thr Asn Gly Asn Gly Phe Thr Thr Gly Thr Thr Gln Thr Val
        35                  40                  45

Thr Val Asp Val His His Gln Leu Gly Gly Gly Gly Gly Gly Ala Ala
    50                  55                  60

Ala Ala Ala Lys Gln Leu Met Ala Asn Gly Ile Ser Gly His Ser Arg
65                  70                  75                  80

Ser Ser Ser Met Ser His Asn Ile His Ala Ala Ala Tyr Ser Glu Leu
                85                  90                  95

Ser Ala Ala Pro Pro Ala Phe Ala Thr Pro Pro Thr Arg Arg Arg Phe
            100                 105                 110

Phe Asn His Lys Asn Leu Arg Ser Ala Leu Thr Gly Gly Ser Gly Gly
        115                 120                 125

Gly Ser Gly Val Gly Gly Gly Val Gly Gly Ala Gly Gly Val Gly Gly
    130                 135                 140

Gly His Arg Arg Thr Ala Ser Asn Gly Gly Cys Pro Ile Asp Thr Ala
145                 150                 155                 160

Ser Ile Leu Ser Gly Asp His Thr His Gln His His His Arg Asp Asn
                165                 170                 175

Gln Pro Glu Gly Lys Glu Ser Asn Ala Leu Asn Thr Ser Thr Cys Ser
            180                 185                 190

Asp Ser Ala Val Thr Arg Arg Arg Arg Lys Asn Val Ser Asn His Asn
        195                 200                 205

Leu Lys Thr Ser Ala Arg His Gly Ala Ser Ser Glu Asn Arg Leu Asn
    210                 215                 220

Arg Leu Ser Leu Ala Gly Thr Ser Val Tyr Ala Gly His Leu Ser Ser
225                 230                 235                 240

Leu Val Phe Gly Lys Ile Lys Ser Leu Trp Ser Val Asn Ser Ser Asn
                245                 250                 255

Ser Ser Glu Ala Gly Leu Asn Gln Leu Ala Gly Met Asp Pro Ile Leu
            260                 265                 270

Leu Arg Ser Asp Ala Ile Asp His His Ser Ser Phe Leu Asn Glu Lys
        275                 280                 285

Leu Gln Lys Asp Gln Leu His Ala Arg Leu Gly Leu Leu Leu Asn Asp
    290                 295                 300

Pro Gly Ser Asn Gly Asn Ser Ser Ser Ser Gly Ser Gly Cys Glu Pro
305                 310                 315                 320

Ile Ser Ala His Ser Thr Thr Ser Thr Thr Ser Ser Ser Gly Val Gly
                325                 330                 335

Ala Ala Ser Thr Thr Thr Ser Gly Ser Ser Gln Asn Val Ser Pro Glu
            340                 345                 350
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Gln Thr Leu Ala Ser Gly Ala Gly Met Leu Ser Gly Ser Gln Leu Ser
355 360 365

Val Ala Thr Ser His Gly Val Lys Glu Asp Ala Leu Ser Leu Cys Gly
370 375 380

Lys Phe Lys Ala Gly Cys Ser Met Leu His Val Tyr Glu Ala Leu Pro
385 390 395 400

Ser Lys Ser Arg Lys Gly Asn Val Arg Arg Ser Thr Arg Gly Gln Gln
405 410 415

Gly Ser Ser Ser Ser Ala Ser Ala Ala Ser Ala Val Gly Ser Arg Val
420 425 430

Thr Ala Ser Ser Leu Ala Ala Val Gln Leu Ala Leu Lys Pro Leu Phe
435 440 445

Phe Glu Val Pro Leu Gln Glu Pro Asp Pro Pro Tyr Val Gly Arg Gln
450 455 460

Trp Leu Val Gln Gln Leu Ser Asn Ile Leu Leu Gly Thr Glu Thr Arg
465 470 475 480

Val Val Leu Ile Asn Gly Gln Pro Gly Thr Gly Lys Thr Ala Phe Cys
485 490 495

Leu Gln Leu Val Glu Tyr Ser Cys Phe Gly Arg Arg Gln Met Gln Asp
500 505 510

Asp Pro Asp Gly Ile Tyr Ser Gln Leu Gln Leu Gly Ala His Cys Glu
515 520 525

Arg Met Arg Gly Leu Ala Ser His Met Val Gly Tyr His Phe Cys Gln
530 535 540

Ala Asp Ala Asn Leu Thr Cys Gln Val Pro Asp Phe Val His Ser Leu
545 550 555 560

Ala Ala Gln Leu Cys Gln Ala Pro Gln Leu Thr Ala Tyr Arg Asp Tyr
565 570 575

Leu Leu Ser Glu Pro His Leu Gln Asp Ile Leu Ser Val Arg Glu Cys
580 585 590

Ile Ala Asp Ala Glu Arg Val Met Lys Leu Ala Ile Leu Glu Pro Leu
595 600 605

Ala His Leu His Arg Ala Gly Lys Ile Pro Ala Lys Val Ala Val Ile
610 615 620

Val Val Asp Ala Leu Cys Glu Ala Glu Tyr His Arg Pro Asp His Gly
625 630 635 640

His Thr Ile Ala Ser Phe Leu Ala Gln Leu Thr Pro His Phe Pro Ala
645 650 655

Trp Leu Lys Leu Val Ala Thr Val Arg Thr Gln Met Leu Glu Leu Val
660 665 670

Lys Ala Pro Ser Tyr Thr Gln Leu Thr Leu Asp Ser Trp Ala Ser Ser
675 680 685

Gln Ala Leu Gln Gln Asp Met Leu Asp Tyr Ile Gly Ala Arg Leu Ala
690 695 700

Asp Ser Pro Glu Ile Arg Met Asn Ile Gly Gly Gly Gly Gly Gln Asn
705 710 715 720

Ser Gln Ser Gly Ser Gln Pro Gln Thr Lys Phe Val Ser His Leu Gln
725 730 735

Ser Leu Ser Arg Gly Ser Met Leu Tyr Ala Lys Leu Ile Leu Asp Leu
740 745 750

Ile Ala Arg Gly Gln Leu Val Ile Lys Ser Ser Ser Tyr Lys Val Leu
755 760 765

Pro Val Ser Leu Ala Gln Ile Phe Leu Leu His Phe Asn Leu Arg Phe
770 775 780

Pro Thr Ala Arg Ser Phe Glu Gln Ala Ala Pro Ile Leu Asn Ile Cys
785 790 795 800

Leu Ala Ala Leu Tyr Pro Leu Thr Leu Asp Glu Ile Tyr Tyr Ser Met
805 810 815

Glu Ala Leu Ser His Gly Arg Glu Ala Leu Ser Trp Pro Asp Phe Met
820 825 830

Gln Arg Phe Lys Leu Leu Asp Gly Phe Leu Ile Lys Arg Leu Asp Asn
835 840 845

Thr Tyr Met Phe Phe His Ser Ser Leu Arg Glu Trp Leu Met Arg Arg
850 855 860

Asp Glu Gly Glu Ser Asn Lys Phe Leu Cys Asp Ala Arg Leu Gly His
865 870 875 880

Ala Gly Ile Ala Phe Arg Leu Ser Arg Leu Gln Ala Pro Leu Ser Pro
885 890 895

Gln Leu Thr Leu Glu Leu Gly His His Met Leu Lys Ala His Leu Tyr
900 905 910

Gly Gly Thr Ser Leu Thr Leu Leu Ser Pro Arg Asp Leu Gln Ser Tyr
915 920 925

Trp Leu Ala Gly Ala Ala Asp Asn Ile Ser Ser Ser Leu Gly Ala Leu
930 935 940

Arg Asn Val Tyr Ser Pro Asn Leu Lys Val Ser Arg Leu Val Leu Leu
945 950 955 960

Ala Gly Ala Ser Pro Asn His Arg Thr Asp Tyr Met Gly Gly Ala Pro
965 970 975

Ile Leu Cys Ile Ala Ala His Glu Gly Ile Leu Pro Met Val Ser Leu
980 985 990

Leu Leu Glu Phe Gly Ala Asp Val Gly Leu Thr Asn Ser Gln Gly Cys

995 1000 1005

Thr Pro Leu Ile Leu Ala Ala Met Arg Gly His Cys Asp Val Val
1010 1015 1020

Arg Pro Leu Val Ala Ala Gly Ser Ser Leu Gly Gln Leu Asp Ile
1025 1030 1035

Thr Gln Arg Cys Ala Leu Val His Ala Ala Arg Met Gly His Leu
1040 1045 1050

Ser Val Val Lys Tyr Leu Leu Ala Cys Asp Trp Ser Pro Arg Pro
1055 1060 1065

His Ser Gln Asp Val Thr Arg Ser Val Ala Leu Gln Gln Ala Leu
1070 1075 1080

Ile Gly Ala Ala Ala Gln Ala His Cys Lys Ile Leu Glu Asp Leu
1085 1090 1095

Leu Asp Leu Asn Glu Thr Glu Phe Asp Leu Asp Val Asn Gly Met
1100 1105 1110

Glu Pro Ser Ser Gly Glu Leu Ala Leu Thr Ala Ala Ala Arg His
1115 1120 1125

Gly Cys Ile Asp Val Val Gly Ile Leu Leu Ser Arg Gly Ala Gln
1130 1135 1140

Ile Asp Ala Arg Asn Arg Gln Gly Tyr Ser Ala Leu Trp Leu Ala
1145 1150 1155

Val Lys Glu Gly His Trp Ser Val Val Glu His Leu Leu Gln Arg
1160 1165 1170

Gly Ala Leu Leu Asp Glu Pro Leu Gly Gln Thr Arg Lys Thr Pro
1175 1180 1185

Leu Met Ile Ala Ala Glu Glu Gly His Leu Glu Leu Val Asp Leu
1190 1195 1200

Leu Leu Ala Arg Gly Ala Gln Arg Glu Ala Gln Asp His Glu Gly
1205 1210 1215

Phe Thr Ala Leu Ser Trp Ala Cys Leu Arg Gly His Leu Ala Ala
1220 1225 1230

Ala Lys Thr Leu Ile Glu His Gly Cys Asn Arg His His Glu Asp
1235 1240 1245

His Asn Gly Arg Thr Ala Leu Asp Leu Ala Ala Tyr Gln Gly Ala
1250 1255 1260

Ala Ser Leu Val Ile Tyr Ile Leu Glu Gln Gly Gly Asn Leu Glu
1265 1270 1275

His Ile Asp Val His Gly Met Arg Pro Leu Asp Arg Ala Ile Ala
1280 1285 1290

Cys Arg Asn Ile Gln Ala Val Gln Val Phe Leu Arg Lys Gly Ala
1295 1300 1305

Lys Leu Gly Pro Thr Thr Trp Ser Met Ala Met Gly Lys Pro Glu
1310 1315 1320

Ile Leu Val Ile Leu Leu Asn Lys Leu Leu Glu Asp Gly Asn Val
1325 1330 1335

Leu Tyr Arg Lys Asn Arg Phe Gln Glu Ala Ala His Arg Tyr Gln
1340 1345 1350

Tyr Ala Leu Arg Lys Ile Ser Gly Leu Glu Gln Leu Leu Glu Arg
1355 1360 1365

Asn Ala Ile Phe Ala Gln Leu Arg Thr Asn Leu Leu Leu Asn Leu
1370 1375 1380

Ser Arg Cys Lys Arg Lys Leu Asn Glu Leu Asp Ala Ser Ile Asp
1385 1390 1395

Leu Ala Thr Gln Ala Ile Ala Gln Lys Pro His Ser Tyr Glu Gly
1400 1405 1410

Tyr Tyr Ala Arg Ala Lys Ala Arg Met Glu Leu Gly Ala Leu Asn
1415 1420 1425

Glu Ala Leu Val Asp Ala Asn Glu Ala Met Gln Gln Ala Ala Gln
1430 1435 1440

Ser Gly Val Leu Cys Glu Val Val Glu Val Leu Lys Arg Ile Gln
1445 1450 1455

Thr Glu Leu Leu Thr Arg Ile Ser Ile Ser Ser Glu Asp Gln Thr
1460 1465 1470

Gly Arg Met Ser Asn Ile Gly Gly Gly Ala Ser Val Ala Tyr Glu
1475 1480 1485

Ser His His Glu Ile Thr Asp Leu
1490 1495

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<211> 336
<212> DNA
<213> Drosophila melanogaster

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ggccgctttc gtctcatgcc cacgtctaat tatggcgcca tttcgccaat cctccagcgg 180

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ccgccgggcg gccgaacagc gcgttctcca tcgcccgaat gggacttcga catcgagcag 300

gtgagtgttc ccagttcctc ggctgggatt gattga 336

<210> 22
<211> 111

<212> PRT
<213> Drosophila melanogaster

<400> 22

Met Gln Ser Ser Ala Gly Gly Ala Ser Gly Gly Ser Asn Tyr Glu Asp
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Val Ala Ala Ala Arg Arg Gly Arg Phe Arg Val Thr Ser Ser Thr Pro
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Gln Gly Pro Pro Glu Thr Thr Leu Gly Arg Phe Arg Leu Met Pro Thr
35 40 45

Ser Asn Tyr Gly Ala Ile Ser Pro Ile Leu Gln Arg Gly Arg Phe Ala
50 55 60

Val Ile Pro Glu Glu Pro Gln Ala Gly Ser Pro Ala Leu Gly Thr Pro
65 70 75 80

Pro Pro Gly Gly Arg Thr Ala Arg Ser Pro Ser Pro Glu Trp Asp Phe
85 90 95

Asp Ile Glu Gln Val Ser Val Pro Ser Ser Ser Ala Gly Ile Asp
100 105 110

<210> 23
<211> 1587
<212> DNA
<213> Drosophila melanogaster

<400> 23
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gcggcgtcgg gagcaacagc aaccgcacca gctgatcgcg tcgaatggtc gcgctcgacg 180

atcttgaact tcatcgagga ctatcgccgg cagcgagtcc tttgggatcc caataccaaa 240

ggttaccaca ttaaacagac caaatacgag gcactcaagc tcctgagtca gaaatatggc 300

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cacggtaagg tcctgagtgg acgaaatcgc ggcgttatct atcagcccat gtggtttgcc 420

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caacagcagc agcaacacga tgagcttacc gctcgcattg cggccactgt ggccgccgtt 660

gctgccgctg cggctgcagc aaacgctcga gatcgggagc gggatgtgga taccgctggc 720

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caacattcca gtaacatggc acaaaaacgt gatcgtgatc gtgatctctc aacgtcaaat 1260

ggcaacggca acagcagcaa caccaataac acctccctgg aaccaatagc aacatccagc 1320

aactgcagtt cgagcagcag caacaacagc gctgccacgc cccccaagcc gctgttgggg 1380

ggcggcggac tgagtgccaa tcatgtggac gaatatggtg tattcgggga atacgtggcc 1440

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aatctgctct atgaagccga actgggtaaa tacgatcatg ggatgccggc cagcaaggag 1560

ccaccgcagt tgtacaatat gcaataa 1587

<210> 24
<211> 528
<212> PRT
<213> Drosophila melanogaster

<400> 24

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Asn Ala Ile Ala Leu Ile Ala Asp Val Ala Thr Leu Pro Leu Pro Leu
20 25 30

Ser Pro Thr Ala Thr Thr Thr Thr Ala Ala Ser Gly Ala Thr Ala Thr
35 40 45

Ala Pro Ala Asp Arg Val Glu Trp Ser Arg Ser Thr Ile Leu Asn Phe
50 55 60

Ile Glu Asp Tyr Arg Arg Gln Arg Val Leu Trp Asp Pro Asn Thr Lys
65 70 75 80

Gly Tyr His Ile Lys Gln Thr Lys Tyr Glu Ala Leu Lys Leu Leu Ser
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Gln Lys Tyr Gly Thr Glu Ile Arg Ser Ile Arg Ser Lys Ile Lys Ser
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Leu Arg Ser Ser Phe His Arg Glu His Gly Lys Val Leu Ser Gly Arg
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Asn Arg Gly Val Ile Tyr Gln Pro Met Trp Phe Ala Tyr Glu Ala Ile
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Arg Phe Ile Leu Asp Gly Glu Arg Asp Gln Asp Arg Asp Gln Asp Gln

145 150 155 160

Asp Gln Asp Ala Glu Thr Glu Thr Glu Val Asp Glu Lys Leu Ala Leu
165 170 175

Met His Ser Leu Asp Leu Glu Gln Leu Lys Ala Asp Lys Leu Val Asp
180 185 190

Arg Asp Ile Ile Leu Gln Val Glu Gln Gln Gln Gln His Asp Glu
195 200 205

Leu Thr Ala Arg Ile Ala Ala Thr Val Ala Ala Val Ala Ala Ala Ala
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Ala Ala Ala Asn Ala Arg Asp Arg Glu Arg Asp Val Asp Thr Ala Gly
225 230 235 240

Asp Met Asp Thr Thr Arg Glu Leu Glu Leu Glu Glu Ala Ala Val Gly
245 250 255

Gly Gly Leu Ile Glu Ser Ser Ser Ala Ala Val Leu Gly Met Leu Asp
260 265 270

Arg Arg Thr Ser Thr Pro Ser Pro Ile Asn Tyr Tyr Lys Pro Thr Asp
275 280 285

Leu Thr Tyr Asn His Arg Lys Arg Lys Ala Met Gly Val Glu His Val
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Val Gly Ala Leu Thr Leu Thr Pro Ile Lys Val Val Gly Gly Ala Val
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Gly Ala Gly Thr Val Gly Ser Ala Gly His Gln Gln Gln Gln Gln His
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Gln Gln Gln Gln Met Asn His Ser Gln Leu Ala Phe Gln Ala Leu Gln
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Gln His Phe Ser His Asn His Gly Leu Ser Leu Ser His Cys Asn Gly
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Gln Pro Gln Gln Gln Gln Gln Gln His Gln His Gln Pro His His Gln
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Gln Gln Gln Gln Gln Gln Ala Leu His Leu Gln His Gln Gln Gln Gln
385 390 395 400

Gln His Ser Ser Asn Met Ala Gln Lys Arg Asp Arg Asp Arg Asp Leu
405 410 415

Ser Thr Ser Asn Gly Asn Gly Asn Ser Ser Asn Thr Asn Asn Thr Ser
420 425 430

Leu Glu Pro Ile Ala Thr Ser Ser Asn Cys Ser Ser Ser Ser Ser Asn
435 440 445

Asn Ser Ala Ala Thr Pro Pro Lys Pro Leu Leu Gly Gly Gly Gly Leu
450 455 460

Ser Ala Asn His Val Asp Glu Tyr Gly Val Phe Gly Glu Tyr Val Ala
465 470 475 480

Ile Thr Ile Arg Lys Leu Lys Thr Ser Lys Ser Lys Ile Val Val Lys
485 490 495

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gcgacagcgg gtagcagtcc ggccaatccc tcatcgggag cccaacagtt ctacgagccg 1020

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<212> PRT
<213> Drosophila melanogaster

<400> 26

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Phe Asp Ser Lys Asp Ala Asn Thr Thr Tyr Thr Gly Asn Cys Ala Pro
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Glu Ser Leu Glu Glu Gln Gln Gln Gln Gln Ser Pro Ser Glu Pro
    50                  55                  60

Ala Val Glu Ser Asn Asn Asn His Ile Val Leu Glu Ala Ser Met Asp
65                  70                  75                  80

Ala Leu Lys Pro Thr Glu Pro Ser Ile Ser Asn Gly His Glu Val Thr
                85                  90                  95

Thr Ala Val Ala Ala Met Lys Ser Gln Ala Glu Val Pro Leu Pro Pro
            100                 105                 110

Thr Ala Ser Ala Ala Ile Pro Glu Asp Ser Ile Ala Arg Leu Glu Val
        115                 120                 125

Val Thr Ser Ala Val Pro Cys Glu Pro Trp Thr Ser Asn Gly Pro Thr
    130                 135                 140

Thr Pro Ser Ala Val Ala Gly Pro Ala Ala Ser Ala Glu Pro Val Asp
145                 150                 155                 160

Cys Ile Ser Lys Leu Gln Ala Val Ala Val Pro Ser Asp Pro Trp Gly
                165                 170                 175

Ser Ile Ala Thr Arg Ser Thr Leu Ala Thr Thr Leu Leu Ser Ala Asp
            180                 185                 190

Glu Leu Asp Asp Asp Asp Asp Asp Phe Glu Asp Asp Tyr Glu Glu Glu
        195                 200                 205

Glu Ser Ile Ile Pro Thr Tyr Cys Pro Met Arg Tyr His Pro Phe Val
    210                 215                 220

Pro His Pro His Pro His Ser His Gln Leu Pro Ser His Pro His Gln
225                 230                 235                 240

Gln Gln Pro Gln Gln Leu Ser Gln Gln Gln Pro His Pro Gln Gln Gln
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Gln Leu Ala Gln Gln Gln Gln Gln His Pro Gln Gln Gln Arg Ser Tyr
            260                 265                 270

Ala Pro Gly Tyr Gly Ser Arg Gln Pro Asn Tyr Tyr Ser Glu Pro Phe
        275                 280                 285

Pro Gln Gln Asn Cys Ser Arg Thr Gly Gly Pro Gln His Met Thr Gln
    290                 295                 300

Ser Pro Pro Thr Pro Gln Gln Ala Arg Gly Phe Ala Pro Pro Gln Trp
305                 310                 315                 320

Ala Thr Ala Gly Ser Ser Pro Ala Asn Pro Ser Ser Gly Ala Gln Gln
                325                 330                 335

Phe Tyr Glu Pro Thr Asn Gly Gly Ala Tyr Ala Pro Pro Ala Ala Pro
            340                 345                 350

Gln Gln Thr Ile Arg Cys Ala Glu Asn Gly Lys Ser Tyr Leu Asp Leu
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Gly Cys Ser Ser Gly Ala Ser Gly Asn Ala Gly Gly Ser Pro Ile Ser
370 375 380

Pro Pro Pro Ser Ser Ala Pro Val Val Pro Phe Ala Gly Leu Pro Leu
385 390 395 400

His Gly Leu Pro Leu Lys Arg Cys Cys Asp Gly Arg Pro Gly Gly Trp
405 410 415

Cys Ser Ala Asn Arg Ser Cys Tyr Lys Asp Thr Arg Leu Lys Ile Arg
420 425 430

Asn Leu Ser Met Phe Lys Leu Ser Arg Phe Arg Gln Val Ser Glu Gln
435 440 445

Ser Leu Tyr Arg Ser Val Leu Ile Cys Asn Thr Leu Lys Arg Ile Asp
450 455 460

Arg Glu Ile Glu Ala Glu Ala Lys Glu Leu His Gln Ala Ala Gln Gln
465 470 475 480

His His Gln Gln Ala Ala Ala Ala Ala Ala Ala Ala Ala Ala Ala Ala
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Ala Gln Ala Ala Gln Tyr His Pro Ala Tyr Gln Gln Gln Gln Gln Gln
500 505 510

Gln Gln Ser Pro Pro Ala Pro Leu His Pro His Thr Gln Gln Gln Met
515 520 525

Asp Tyr Ala Pro Val Leu Asn Cys Ala Arg Leu Ala Asn Met Asp His
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Tyr Gln Gln Leu Ser Phe Gln Pro Gln His Gln Gln Gln Gln Gln Pro
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Ser Gln Pro His Ser Tyr His Glu Arg Leu Asp Ser Gln Pro Ala Tyr
565 570 575

Arg Gly Ala Ala Ala Gly Ala Gly Ser Phe Ala Thr Gln Pro Ser Asn
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Cys Asp Thr Ser Ala Gly Ala Ser Ser Ser Asn Thr Ser Gly Asn Ser
595 600 605

Asn Asn Ser Ser Ala Thr Ala Ala Ser Ser Asn Ser Ser Leu His Pro
610 615 620

Tyr Asp His Tyr Pro Phe Arg Glu Ser Gln Ser Gly Arg Ala Thr Pro
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Phe Pro Ala Cys Pro Thr Thr Thr Ala Ala Ala Ala Ala Ala Ser Ala
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Ala Ala Ala Ala Ser Ser Gly Gly Ala Ala Thr Thr Leu Ser Ser Asn
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Ile Ser Ser Ser Pro Ala Ser Ser Ser Thr Ser Ser Asn Thr Thr Ser
675 680 685

Ser Thr Val Ile Ser Ser Ser Ser Gly Asn Thr Val Ser Ser Asn Gly
690 695 700

Thr Thr Pro Val Ala Pro Thr Ala Ser Ser Ser Asn Cys Asp Thr Ser
705 710 715 720

Asp Ser Gly Tyr Ala Asp Asp Asp Ser Thr Arg Ser Ile Asn Trp Ser
725 730 735

Ser Val Leu Ser Leu Ser Ser Gln Ser Ala Leu Asp Pro Leu Asn Asn
740 745 750

Asn Asp Leu Phe Ser Ile Leu Pro Ser Ala Ala Thr Pro Thr Ala Val
755 760 765

Pro Val Ser Val Pro Ala Ser Ser Ser Ser Ser Ser Ser Gly Ser Thr
770 775 780

Leu Ala Phe Ser Gly Ser Phe Thr Thr Val Gln Ala Ser Gly Gly Ser
785 790 795 800

Ser Ser Ser Cys Gly Ser Ser Ser Thr Thr Ala Thr Phe Thr Thr Leu
805 810 815

Ser Thr Ile Ser Ser Ala Thr His Ser Leu Thr Ser Ser Tyr Val Ser
820 825 830

Ser Ile Ser Ser Asn Val Ser Ala Gly Ala Asn Thr Trp Glu Tyr Gly
835 840 845

Phe Leu Asp Met Glu Phe Gly Leu Gly Ser Glu Phe Thr Glu Leu Val
850 855 860

Pro Ser Cys Lys Leu Ser Ser Glu Asp Leu Phe Lys Ser Gly Leu Gly
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Gly Gln Val Val Thr Ala Ser Arg Leu His Asp Asn Glu Leu Glu His
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Pro Ala His Ile Met Val Gly Ser
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35 40 45

Glu Leu Glu Asn Leu Gly Met Leu Arg Ile Gly His Gln Glu Ile Val
50 55 60

Leu Glu Ala Val Glu Asn Leu Arg Asn Phe His Tyr His Leu Lys Asn
65 70 75 80

Asp Asn Leu Gln Phe Met Ala Leu His Val Ala Thr Ala Ala Lys Asn
85 90 95

Leu His Arg Glu Leu Ala Arg Asn His Ala Glu Ser Thr Lys Ile Asp
100 105 110

Thr Arg Ile Leu His Asp Ile Thr Arg Thr Ile Ala Thr Leu Lys Pro
115 120 125

Leu Val Gly Ser Leu Glu Arg Thr Pro Phe Arg Lys Gln Glu Met Tyr
130 135 140

Arg Glu Tyr Cys Gly Asn Val Leu Lys Cys Gly Leu Glu Leu Ala Thr
145 150 155 160

Ile Ala His Arg Asp Arg Phe Ala Leu Gln Pro Val Pro Ala Ile Arg

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Gln Ser Ala Glu Arg Leu Glu Asn Leu Ala Asn Phe Val Ile Gln Asp
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Ile Ser Asp Pro Met Val Leu Gln Pro Ala Ser Leu Asn Leu Val Thr
        195                 200                 205

Leu Lys Lys Arg Glu Ser Glu Leu Gly Phe Asn Ile Glu Ser Ser Tyr
    210                 215                 220

Asn Gly Ile His Arg Val Thr Asp Ile Lys Tyr Asn Ser Pro Ala His
225                 230                 235                 240

Asn Ser Gly Lys Ile Glu Asp Gly Asp Glu Ile Val Gln Ile Asn Tyr
                245                 250                 255

Gln Thr Val Val Gly Trp Gln His Arg Thr Val Leu Glu His Leu Arg
            260                 265                 270

Glu Ala Leu Pro Asp Val Val Leu Thr Val Lys Lys Arg Pro Lys His
        275                 280                 285

Thr Lys Met Phe Gly Gln Ile Tyr Met Gln Pro Tyr Arg Leu Pro Ser
    290                 295                 300

Lys Lys Arg Asn Met Ala Ala Arg Trp Ala Ala Gln Met Pro Ser Pro
305                 310                 315                 320

Arg Ala Ala Phe Leu Thr Leu Asp Thr Glu Gln Leu Ala Thr Gly Gly
                325                 330                 335

Thr Gly Ser Ala Val Pro Asp Pro Ser Lys Ser Leu Ser Ser Glu Lys
            340                 345                 350

Arg Glu Val Leu Thr Lys Ala Asn Pro Val Ser Ser Ala Ser Asp Ser
        355                 360                 365

Asp Ser Ser Cys Ser Asp Ile Pro Thr Pro Thr Asp Pro Lys Leu Ala
    370                 375                 380

Ala Arg Glu Ile Arg Leu Tyr Tyr Pro Lys Pro Arg Ala Leu Leu Gln
385                 390                 395                 400

Arg Arg Asn Thr Ile Cys Gly Cys Glu Tyr Leu Ser Leu Lys Asn Ser
                405                 410                 415

Asp Leu Val Val Pro Ser Trp His Glu Arg Lys Pro Gly Ile Gly Ser
            420                 425                 430

Pro Thr Asn Cys Asp Pro Gly Ser Pro Ser Ile Arg Asp Lys Ser Ile
        435                 440                 445

Ser Phe Gly Tyr Gly Leu Glu Met Ala Ala Arg Pro Thr Thr Cys Ile
    450                 455                 460

Gly Ile Ala Gly Asp Thr Ser Thr Asp Lys Ala Arg Arg Met Phe His
465                 470                 475                 480

Glu Ala Arg Lys Leu Lys Gln Leu Thr Glu Asp Ser Gln Arg Glu Phe
                485                 490                 495
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Leu Val Asp Arg Tyr Lys Pro Gly Val Ser Lys Val Val Arg Phe Asp
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Ala Lys Glu Asp Tyr Val Met Lys Asn Glu Lys Phe Ile Cys Asn Val
515 520 525

Glu Asn Thr Ile Leu Glu Thr Phe Glu Pro Ile Pro Phe Ala Asp Glu
530 535 540

Gly Asp Glu Asp Ala Leu Glu Thr Leu Arg Asn Cys Lys Thr Glu Asn
545 550 555 560

Ala Glu Glu Leu Leu Glu Ala Ile Asn Leu Ala Thr Lys Gly Gln Asp
565 570 575

Leu Pro Leu Ala Glu Ala Ile Asn Met Pro Leu Leu Gln Gln Gly Arg
580 585 590

Arg Gly Arg Leu Asp Lys Ser His Ser Thr Pro Ala Tyr Asp Asn Ser
595 600 605

Gly Glu Glu Ser Asp Thr Pro Pro Ala Ile Glu Pro Arg Lys Glu Phe
610 615 620

Leu Leu Val Thr Pro Pro Ala Pro Pro Pro Arg Pro Arg Lys Gln Arg
625 630 635 640

Glu Met Thr Pro Pro Ala Val Pro Pro Pro Pro Pro Lys Pro Ala Ser
645 650 655

Met Gln Pro Ala Ser Ser Ile Thr Ser Ile Ser Ile Pro Val Pro Val
660 665 670

Pro Val Pro Ala Ala Val Asp Pro Ser Glu Ile Ser Glu Leu His Thr
675 680 685

Pro Ser Lys Ser Arg Thr Leu Thr Leu Lys Lys Lys His Ser Leu Met
690 695 700

Ala Lys Arg Arg Asn Thr Asn Leu Lys Leu Leu Gly Thr Gly Asp Ile
705 710 715 720

Gln Gly His Leu Tyr Arg Arg Lys Lys Asn His Arg Gly Val Thr Tyr
725 730 735

Trp Ala Arg Ile Tyr Phe Val Met Leu Asp Thr Ile Leu Tyr Gly Phe
740 745 750

Arg Ser Lys Gln Ser Thr Ser Ala Ser Leu Val Ile Phe Leu Pro Gly
755 760 765

Phe Thr Val Ser Leu Ala Lys Glu Val His Ser Lys Pro His Ala Phe
770 775 780

Lys Val Tyr His Thr Ala Lys Ser Phe Tyr Phe Ala Ala Glu Ser Leu
785 790 795 800

Asp Ala Leu Asn Gln Trp Val Asp Phe Leu Arg Gln Ala Ser Leu Lys
805 810 815

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Val Pro Pro Ser Thr Gly Ser Lys Gly Gly Gly Asp Ala Lys Asp Leu
            820                 825                 830

Tyr Ser Glu Asn Asp Ser Ser Gly Glu Glu Cys Asp Ala Leu Val Ile
        835                 840                 845

Gln Asn Leu Ser Thr Pro Ser Pro Gln Gly Asn Lys Glu Ser Met Ser
    850                 855                 860

Met Ser Met Thr Leu Ser Gly Gly Thr Pro Pro Ser Ser Ala Pro Ile
865                 870                 875                 880

Lys His Glu Arg Gly Tyr Leu Asp Ser Phe Arg Lys Phe Thr Asn Thr
                885                 890                 895

Phe Lys Ser Ser Ala Ala Lys Pro Ser Ser Asp Ile Pro Val Pro Thr
            900                 905                 910

Glu Gln Tyr Arg Ser Tyr Arg Lys Val Pro Gly Gly Ser Phe Gly Ile
        915                 920                 925

Gln Ile Gly Ala Asn Thr Pro Gly Tyr His Asp Pro Ala Met Pro Pro
    930                 935                 940

Thr Gln Ile Pro Pro Leu Val Gly Pro Lys Leu Ser Arg Ser Ser Ser
945                 950                 955                 960

Arg Ser Ser Val Val Ser Gly Thr Glu Ser Ala Val Ser Leu Ser Ala
                965                 970                 975

Ser Ile Leu Gly Pro Pro Ala Ser Pro Ala Pro Thr Pro Thr Pro Thr
            980                 985                 990

Ala Thr Pro Thr Ser Leu Gln His  Gln Ser Ser Glu Glu  Ser Pro Ser
        995                 1000                1005

Gln Ser  Gln Ser Gln Ser Pro  Ser Ser Lys Ser Ser  Leu Lys Lys
    1010                1015                1020

Ala Pro  Phe Asn Phe Leu His  Ala Ser Asn Pro Asn  Leu Val Glu
    1025                1030                1035

Phe Asp  Phe His Thr Ser Lys  Thr Leu Leu Pro Lys  Met Ser Val
    1040                1045                1050

Gly Asn  Thr Leu Asp His Gly  His Asn Ile Gln Gly  Phe Val Thr
    1055                1060                1065

Leu Lys  Asp Leu Met Leu Arg  Lys Gln Glu Glu Glu  Ala Gln Glu
    1070                1075                1080

Met Tyr  Asn Asn Arg Val His  Leu Gly Val Glu Lys  His Lys His
    1085                1090                1095

Ala Arg  Thr Glu Ser Thr Ala  Ser Gln Gln Ser Ala  Met Ser Ser
    1100                1105                1110

Ser Val  Thr Lys Pro Leu Glu  Lys Leu Pro Lys Ile  Gln Ser Val
    1115                1120                1125

Ser Leu  Pro Lys Thr Pro Asp  Tyr Glu Ile Ser Phe  Lys Pro Asp
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Asp Glu Ser Ile Lys Arg Thr Arg Thr Lys Glu Gly Gln Lys Leu
1145 1150 1155

Arg Asp Phe Gly Tyr Glu Leu Ile Cys Gly Asp Glu Pro Ser Thr
1160 1165 1170

Ser Ser Ile Ser Arg Gln Glu His His His His His His His His
1175 1180 1185

Gln His His Leu Gln His Val Gln Gln Gln Gln Gln Leu Gln His
1190 1195 1200

Gln Gln Thr Gln Gln Gln His Ser Ser Lys Ala Lys His Phe Leu
1205 1210 1215

Arg Ser Gln Gln Leu Gln Leu Ser Ser Phe Leu His Lys Asn Ser
1220 1225 1230

Ser Gly Gly Ser Gly Lys Ser Ser Gly Ser Gly Ala Asp Gln Lys
1235 1240 1245

Lys Ser Lys Gly Lys Ser Ser Gly Asp Arg Arg Phe Pro Phe Ser
1250 1255 1260

Lys His Ser Thr Gly Ser Ala Gly Ser Gly Cys Gly Pro Gly His
1265 1270 1275

Ala Met Thr Met Thr Leu Pro Leu Asn Lys Lys Ser Lys Ser Asn
1280 1285 1290

His Ala Leu Asp Gly Ala Val Gly Asn Gly Val Thr Ile Ile Gly
1295 1300 1305

Ser Gly Ser Ser Ile Lys Lys Ser Gln Thr Tyr Asn Gln Asp Leu
1310 1315 1320

Arg Asp Lys Ile Val Gly Thr Lys Tyr Asp Ala His Arg Lys Asn
1325 1330 1335

Ser Ala Pro Ile Pro Ile Phe Ser Lys Leu Ser Ile Ser Gly Gly
1340 1345 1350

Thr Pro Ala Lys Pro Ser Lys Glu Asn Arg Phe Leu Gly Ser Pro
1355 1360 1365

Leu Leu His Arg Thr Leu Phe Gly His His His His Gln Gln Gln
1370 1375 1380

Ala Val Thr Pro Pro Ser Ser Ala Asp Pro Asp Cys Asp Gln Glu
1385 1390 1395

Ile Phe Ser Gln Ile Thr Leu Pro Thr His Asn Gln Ala Gly Tyr
1400 1405 1410

Arg Ser Tyr Arg Gly Pro Gly Ile Leu Thr Thr Ser Thr Thr Asn
1415 1420 1425

Leu Cys Ser Ser Glu Gly Leu Gln Pro Pro Leu Pro Pro Ala Pro
1430 1435 1440

Pro Pro Pro Val Asn Thr Ser Arg Gln Arg Glu Glu Glu Gln Ala
1445 1450 1455

Glu Ala Thr Ile Ser Glu Cys Ala Ala Thr Pro Lys Val Ser Ser
1460 1465 1470

Ser Gly Ser Val Asp Ser Lys Ala Ala Thr Pro Asp Tyr Pro Asn
1475 1480 1485

Met Glu Cys Pro Pro Val Phe Glu Pro Glu Ile Tyr Ser Leu Ser
1490 1495 1500

Asp Thr Ser Leu Ser Arg Ile Val Met Arg Thr Pro Ser Ser Ser
1505 1510 1515

Gly Ala Thr Ser Ala Thr Ala Ser Thr Thr Thr Thr Asn Asn Asn
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Asn Asn Asn Asn Asn Thr Asn Asn Asn Thr Asn Thr Asn Ser Ser
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Pro Ser Gly Gly Glu His His Gln Thr
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ttcgacacgc tcacatcacc accagcgccc ggctcgtcgg tcaatcccac cgccgtcacc 240

agcccaagtg cccagaatgt ggccgctggt ggagcaactg tggccggtgc agcagcaact 300

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cgtggctatg tgcatcacta tgacatcaat atacagccgg acaagtgtcc gcgaaaggtg 540

aaccgtgaga ttatcgagac tatggtgcat gcctatagca agatcttcgg agtgctcaag 600

ccggtgttcg atggtcgcaa caatctgtat acccgcgatc ccctgcccat tggcaacgag 660

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atgtactttg cctaa 2955

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<212> PRT
<213> Drosophila melanogaster

<400> 30

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Pro His Thr Leu Pro Leu Thr Phe Pro Asp Leu Gln Met Thr Ser Thr
20 25 30

Val Gly Ile Ile Gly Lys Val Tyr Glu Ser Gln Trp Thr Pro Ser Pro
35 40 45

Thr Arg Pro Gln Ser Pro Ser Gln Ala Gln Thr Ser Phe Asp Thr Leu
50 55 60

Thr Ser Pro Pro Ala Pro Gly Ser Ser Val Asn Pro Thr Ala Val Thr
65 70 75 80

Ser Pro Ser Ala Gln Asn Val Ala Ala Gly Gly Ala Thr Val Ala Gly
85 90 95

Ala Ala Ala Thr Ala Ala Gln Val Ala Ser Ala Leu Gly Ala Thr Thr
100 105 110

Gly Ser Val Thr Pro Ala Ile Ala Thr Ala Thr Pro Ala Thr Gln Pro
115 120 125

Asp Met Pro Val Phe Thr Cys Pro Arg Arg Pro Asn Leu Gly Arg Glu
130 135 140

Gly Arg Pro Ile Val Leu Arg Ala Asn His Phe Gln Val Thr Met Pro
145 150 155 160

Arg Gly Tyr Val His His Tyr Asp Ile Asn Ile Gln Pro Asp Lys Cys
165 170 175

Pro Arg Lys Val Asn Arg Glu Ile Ile Glu Thr Met Val His Ala Tyr
180 185 190

Ser Lys Ile Phe Gly Val Leu Lys Pro Val Phe Asp Gly Arg Asn Asn
195 200 205

Leu Tyr Thr Arg Asp Pro Leu Pro Ile Gly Asn Glu Arg Leu Glu Leu
210 215 220

Glu Val Thr Leu Pro Gly Glu Gly Lys Asp Arg Ile Phe Arg Val Thr
225 230 235 240

Ile Lys Trp Gln Ala Gln Val Ser Leu Phe Asn Leu Glu Glu Ala Leu
245 250 255

Glu Gly Arg Thr Arg Gln Ile Pro Tyr Asp Ala Ile Leu Ala Leu Asp
260 265 270

Val Val Met Arg His Leu Pro Ser Met Thr Tyr Thr Pro Val Gly Arg
275 280 285

Ser Phe Phe Ser Ser Pro Glu Gly Tyr Tyr His Pro Leu Gly Gly Gly
290 295 300

Arg Glu Val Trp Phe Gly Phe His Gln Ser Val Arg Pro Ser Gln Trp
305 310 315 320

Lys Met Met Leu Asn Ile Asp Val Ser Ala Thr Ala Phe Tyr Lys Ala
325 330 335

Gln Pro Val Ile Asp Phe Met Cys Glu Val Leu Asp Ile Arg Asp Ile
340 345 350

Asn Glu Gln Arg Lys Pro Leu Thr Asp Ser Gln Arg Val Lys Phe Thr
355 360 365

Lys Glu Ile Lys Gly Leu Lys Ile Glu Ile Thr His Cys Gly Gln Met
370 375 380

Arg Arg Lys Tyr Arg Val Cys Asn Val Thr Arg Arg Pro Ala Gln Met
385 390 395 400

Gln Ser Phe Pro Leu Gln Leu Glu Asn Gly Gln Thr Val Glu Cys Thr
405 410 415

Val Ala Lys Tyr Phe Leu Asp Lys Tyr Arg Met Lys Leu Arg Tyr Pro
420 425 430

His Leu Pro Cys Leu Gln Val Gly Gln Glu His Lys His Thr Tyr Leu
435 440 445

Pro Leu Glu Val Cys Asn Ile Val Ala Gly Gln Arg Cys Ile Lys Lys
450 455 460

Leu Thr Asp Met Gln Thr Ser Thr Met Ile Lys Ala Thr Ala Arg Ser
465 470 475 480

Ala Pro Asp Arg Glu Arg Glu Ile Asn Asn Leu Val Lys Arg Ala Asp
485 490 495

Phe Asn Asn Asp Ser Tyr Val Gln Glu Phe Gly Leu Thr Ile Ser Asn
500 505 510

Ser Met Met Glu Val Arg Gly Arg Val Leu Pro Pro Pro Lys Leu Gln
515 520 525

Tyr Gly Gly Arg Val Ser Thr Gly Leu Thr Gly Gln Gln Leu Phe Pro
530 535 540

Pro Gln Asn Lys Val Ser Leu Ala Ser Pro Asn Gln Gly Val Trp Asp
545 550 555 560

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Met Arg Gly Lys Gln Phe Phe Thr Gly Val Glu Ile Arg Ile Trp Ala
                565                 570                 575

Ile Ala Cys Phe Ala Pro Gln Arg Thr Val Arg Glu Asp Ala Leu Arg
            580                 585                 590

Asn Phe Thr Gln Gln Leu Gln Lys Ile Ser Asn Asp Ala Gly Met Pro
        595                 600                 605

Ile Ile Gly Gln Pro Cys Phe Cys Lys Tyr Ala Thr Gly Pro Asp Gln
    610                 615                 620

Val Glu Pro Met Phe Arg Tyr Leu Lys Ile Thr Phe Pro Gly Leu Gln
625                 630                 635                 640

Leu Val Val Val Val Leu Pro Gly Lys Thr Pro Val Tyr Ala Glu Val
                645                 650                 655

Lys Arg Val Gly Asp Thr Val Leu Gly Met Ala Thr Gln Cys Val Gln
            660                 665                 670

Ala Lys Asn Val Asn Lys Thr Ser Pro Gln Thr Leu Ser Asn Leu Cys
        675                 680                 685

Leu Lys Ile Asn Val Lys Leu Gly Gly Ile Asn Ser Ile Leu Val Pro
    690                 695                 700

Ser Ile Arg Pro Lys Val Phe Asn Glu Pro Val Ile Phe Leu Gly Ala
705                 710                 715                 720

Asp Val Thr His Pro Pro Ala Gly Asp Asn Lys Lys Pro Ser Ile Ala
                725                 730                 735

Ala Val Val Gly Ser Met Asp Ala His Pro Ser Arg Tyr Ala Ala Thr
            740                 745                 750

Val Arg Val Gln Gln His Arg Gln Glu Ile Ile Gln Glu Leu Ser Ser
        755                 760                 765

Met Val Arg Glu Leu Leu Ile Met Phe Tyr Lys Ser Thr Gly Gly Tyr
    770                 775                 780

Lys Pro His Arg Ile Ile Leu Tyr Arg Asp Gly Val Ser Glu Gly Gln
785                 790                 795                 800

Phe Pro His Val Leu Gln His Glu Leu Thr Ala Ile Arg Glu Ala Cys
                805                 810                 815

Ile Lys Leu Glu Pro Glu Tyr Arg Pro Gly Ile Thr Phe Ile Val Val
            820                 825                 830

Gln Lys Arg His His Thr Arg Leu Phe Cys Ala Glu Lys Lys Glu Gln
        835                 840                 845

Ser Gly Lys Ser Gly Asn Ile Pro Ala Gly Thr Thr Val Asp Val Gly
    850                 855                 860

Ile Thr His Pro Thr Glu Phe Asp Phe Tyr Leu Cys Ser His Gln Gly
865                 870                 875                 880

Ile Gln Gly Thr Ser Arg Pro Ser His Tyr His Val Leu Trp Asp Asp
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885 890 895

Asn His Phe Asp Ser Asp Glu Leu Gln Cys Leu Thr Tyr Gln Leu Cys
900 905 910

His Thr Tyr Val Arg Cys Thr Arg Ser Val Ser Ile Pro Ala Pro Ala
915 920 925

Tyr Tyr Ala His Leu Val Ala Phe Arg Ala Arg Tyr His Leu Val Glu
930 935 940

Lys Glu His Asp Ser Gly Glu Gly Ser His Gln Ser Gly Cys Ser Glu
945 950 955 960

Asp Arg Thr Pro Gly Ala Met Ala Arg Ala Ile Thr Val His Ala Asp
965 970 975

Thr Lys Lys Val Met Tyr Phe Ala
980

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<212> DNA
<213> Drosophila melanogaster

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gcccccttccc agttgccagc cggcgaccag gatgcggatc tagacaccct gaaggcggcg 180

gccacgggca tgcgtacccg atccggacgc actgcccgac taattgtcac cgccgctcaa 240

gagagcaaaa agaagacacc ggctgccgcc aagatggagc cacacatcaa gcagcccaag 300

ctggtgcaat tcattaaaaa gggcactctg tcgcccagga aacaggctca gtccagtaag 360

ctggacgagg aggagctgca gcagtcgtcg gccataagcg agcacacgcc caaggttaac 420

ttcaccatca caagccagca gaatgcggac aatgtgcagc gtggcctgcg cacacccacc 480

aagcagatcc tcaaggatgc ctcgccgatc aaggcggatc tccgccgtca gctcactttc 540

gacgaggtaa aaacgaaggt atcgcggagt gccaagctgc aggaactcaa ggcagtgctg 600

gcccttaagg cggcgctcga gcagaagcgc aaggagcagg aggagcgcaa caggaaactc 660

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acaatcgaac tggaggtgct tataagccct ttgaagacct tcaagactcc cacaaaaata 780

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acaccgcagg aaattgaggc gcatctgaaa ctacttgcca aggagctacc cagctgggct 2040

tcctttcatg aagtgcgcaa gaccatgtac ctcaaggttg ccaaggacat ggacatgaac 2100

aagatcatcg agaagctgga gagcgtggct aacgccaaga gcaattag 2148

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<211> 715
<212> PRT
<213> Drosophila melanogaster

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Ala Glu Thr Val Ser Pro Ala Ser Ala Pro Ser Gln Leu Pro Ala Gly
35 40 45

Asp Gln Asp Ala Asp Leu Asp Thr Leu Lys Ala Ala Ala Thr Gly Met
50 55 60

Arg Thr Arg Ser Gly Arg Thr Ala Arg Leu Ile Val Thr Ala Ala Gln
65 70 75 80

Glu Ser Lys Lys Lys Thr Pro Ala Ala Ala Lys Met Glu Pro His Ile

85 90 95

Lys Gln Pro Lys Leu Val Gln Phe Ile Lys Lys Gly Thr Leu Ser Pro
100 105 110

Arg Lys Gln Ala Gln Ser Ser Lys Leu Asp Glu Glu Glu Leu Gln Gln
115 120 125

Ser Ser Ala Ile Ser Glu His Thr Pro Lys Val Asn Phe Thr Ile Thr
130 135 140

Ser Gln Gln Asn Ala Asp Asn Val Gln Arg Gly Leu Arg Thr Pro Thr
145 150 155 160

Lys Gln Ile Leu Lys Asp Ala Ser Pro Ile Lys Ala Asp Leu Arg Arg
165 170 175

Gln Leu Thr Phe Asp Glu Val Lys Thr Lys Val Ser Arg Ser Ala Lys
180 185 190

Leu Gln Glu Leu Lys Ala Val Leu Ala Leu Lys Ala Ala Leu Glu Gln
195 200 205

Lys Arg Lys Glu Gln Glu Glu Arg Asn Arg Lys Leu Arg Asp Ala Gly
210 215 220

Pro Ser Pro Ser Lys Ser Lys Met Ser Val Gln Leu Lys Glu Phe Asp
225 230 235 240

Thr Ile Glu Leu Glu Val Leu Ile Ser Pro Leu Lys Thr Phe Lys Thr
245 250 255

Pro Thr Lys Ile Pro Pro Pro Thr Pro Asp Lys His Glu Leu Met Ser
260 265 270

Pro Arg His Thr Asp Val Ser Lys Arg Leu Leu Phe Ser Pro Ala Lys
275 280 285

Asn Gly Ser Pro Val Lys Leu Val Glu Val Pro Ala Tyr Lys Arg Tyr
290 295 300

Ala Ser Leu Val Glu Ser Ser Arg Ala Gly Gln Leu Pro Leu Pro Tyr
305 310 315 320

Lys Tyr Arg His Leu Leu Asp Val Phe Lys Gly Leu Asp Ser Val Val
325 330 335

Ala Met Phe His Asn Arg Lys Glu Thr Ile Thr Phe Lys Lys Leu Lys
340 345 350

Pro Ala Val Gln Arg Met Leu Arg Lys Asn Phe Thr Glu Thr His Leu
355 360 365

Ala Gln Ile Lys His Ile Tyr Pro Asp Ala Phe Ile Phe Ser Gln Val
370 375 380

Lys Thr Arg Asn Phe Gly Ser Val Ser Lys Ala Asp Tyr Phe Gln Leu
385 390 395 400

Ile Ile Ala Pro Asn Val Glu Pro Leu Pro Glu Gln Gln Gln Ser Glu
405 410 415

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Lys Pro Gln His Phe Thr Lys Ile Asn Glu Asp Asp Val Leu Ala Ser
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Ala Gln Ser Thr Ser Met Asn Pro His Asp Pro Pro Ile Ile Ile Glu
        435                 440                 445

Lys Ala Leu Thr Arg Trp His Pro Gln Phe Asp Leu Glu Ser Cys Pro
    450                 455                 460

Glu Val Glu Leu Ser Pro Leu Pro Gln Pro Pro Asn Val Glu Lys Tyr
465                 470                 475                 480

Ser Ser Ala Lys Asp Ile Leu Ser Thr Ala Arg Asn Leu Phe Asn Cys
                485                 490                 495

Ala Thr Pro Met Glu Arg Ala Met Asp Arg Tyr Glu Ala Lys Leu Glu
            500                 505                 510

Ser Glu Lys Gln Gln Ala Ala Glu Ser Asn Lys Lys Thr Glu Glu Gln
        515                 520                 525

Gln Ala Gly Glu Val Thr Arg Thr Ser Thr Ala Ile Gln Thr Ser Gln
    530                 535                 540

Glu Val Pro Gly Ile Ser Gly Ser Ser Lys Asn Pro Thr Val Pro Glu
545                 550                 555                 560

Thr Thr Asn Gln Thr Glu Thr Ala Lys Pro Thr Val Lys Asp Cys Thr
                565                 570                 575

Val Pro Asp Ala Ser Ser Asn Leu Leu Lys Gly Leu Pro Lys Ser Leu
            580                 585                 590

Ile Glu Lys Ile Arg Ala Lys Gln Ala Ala Lys Ala Leu Glu Ala Met
        595                 600                 605

Thr Arg Arg Pro Ser Gln Asp Gln Glu Ala Thr Lys Tyr Ser Arg Leu
    610                 615                 620

Pro Glu Leu Ala Arg His Leu Arg Asn Val Phe Val Thr Glu Arg Lys
625                 630                 635                 640

Gly Val Leu Thr Leu Glu Val Ile Ile Lys Lys Ile Gln Asn Ser Phe
                645                 650                 655

Arg Ala Asn Leu Thr Pro Gln Glu Ile Glu Ala His Leu Lys Leu Leu
            660                 665                 670

Ala Lys Glu Leu Pro Ser Trp Ala Ser Phe His Glu Val Arg Lys Thr
        675                 680                 685

Met Tyr Leu Lys Val Ala Lys Asp Met Asp Met Asn Lys Ile Ile Glu
    690                 695                 700

Lys Leu Glu Ser Val Ala Asn Ala Lys Ser Asn
705                 710                 715
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<212> DNA

<213> Drosophila melanogaster

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Ser Asn Asn Gly Ser Asp Pro Ser Ile Gln Gln Gln Gln Asn Val
    50                  55                  60

Ala Pro His Pro Tyr Gly Ala Pro Pro Pro Pro Gly Ser Gly Pro Gly
65                  70                  75                  80

Gly Pro Pro Gly Pro Asp Pro Ala Ala Val Met His Tyr His His Leu
                85                  90                  95

His Gln Gln Gln Gln Gln His Pro Pro Pro Pro His Met Gln Gln Gln
            100                 105                 110

Gln His His Gly Gly Pro Ala Pro Pro Pro Pro Gly Gly Ala Pro Glu
        115                 120                 125

His Ala Pro Gly Val Lys Glu Glu Tyr Thr His Leu Pro Pro Pro His
    130                 135                 140

Pro His Pro Ala Tyr Gly Arg Tyr His Ala Asp Pro Asn Met Asp Pro
145                 150                 155                 160

Tyr Arg Tyr Gly Gln Pro Leu Pro Gly Gly Lys Pro Pro Gln Gln Gln
                165                 170                 175

Gln Pro His Pro Gln Gln Gln Pro Pro Gln Gln Pro Gly Pro Gly Gly
            180                 185                 190

Ser Pro Asn Arg Pro Pro Gln Gln Arg Tyr Ile Pro Gly Gln Pro Pro
        195                 200                 205

Gln Gly Pro Thr Pro Thr Leu Asn Ser Leu Leu Gln Ser Ser Asn Pro
    210                 215                 220

Pro Pro Pro Pro Gln His Arg Tyr Ala Asn Thr Tyr Asp Pro Gln Gln
225                 230                 235                 240

Ala Ala Ala Ser Ala Ala Ala Ala Ala Ala Ala Gln Gln Gln Gln Ala
                245                 250                 255

Gly Gly Pro Pro Pro Pro Gly His Gly Pro Pro Pro Pro Gln His Gln
            260                 265                 270

Pro Ser Pro Tyr Gly Gly Gln Gln Gly Gly Trp Ala Pro Pro Pro Arg
        275                 280                 285

Pro Tyr Ser Pro Gln Leu Gly Pro Ser Gln Gln Tyr Arg Thr Pro Pro
    290                 295                 300

Pro Thr Asn Thr Ser Arg Gly Gln Ser Pro Tyr Pro Pro Ala His Gly
305                 310                 315                 320

Gln Asn Ser Gly Ser Tyr Pro Ser Ser Pro Gln Gln Gln Gln Gln Gln
                325                 330                 335

Gln Gln Gln Gln Gln Gln Gln Ala Gly Gln Gln Pro Gly Gly Pro Val
            340                 345                 350

Pro Gly Gly Pro Pro Pro Gly Thr Gly Gln Gln Pro Pro Gln Gln Asn
        355                 360                 365
```

```
Thr Pro Pro Thr Ser Gln Tyr Ser Pro Tyr Pro Gln Arg Tyr Pro Thr
    370                 375                 380

Pro Pro Gly Leu Pro Ala Gly Gly Ser Asn His Arg Thr Ala Tyr Ser
385                 390                 395                 400

Thr His Gln Tyr Pro Glu Pro Asn Arg Pro Trp Pro Gly Gly Ser Ser
                405                 410                 415

Pro Ser Pro Gly Ser Gly His Pro Leu Pro Pro Ala Ser Pro His His
            420                 425                 430

Val Pro Pro Leu Gln Gln Gln Pro Pro Pro Pro Pro His Val Ser Ala
        435                 440                 445

Gly Gly Pro Pro Pro Ser Ser Ser Pro Gly His Ala Pro Ser Pro Ser
    450                 455                 460

Pro Gln Pro Ser Gln Ala Ser Pro Ser Pro His Gln Glu Leu Ile Gly
465                 470                 475                 480

Gln Asn Ser Asn Asp Ser Ser Ser Gly Gly Ala His Ser Gly Met Gly
                485                 490                 495

Ser Gly Pro Pro Gly Thr Pro Asn Pro Gln Gln Val Met Arg Pro Thr
            500                 505                 510

Pro Ser Pro Thr Gly Ser Ser Gly Ser Arg Ser Met Ser Pro Ala Val
        515                 520                 525

Ala Gln Asn His Pro Ile Ser Arg Pro Ala Ser Asn Gln Ser Ser Ser
    530                 535                 540

Gly Gly Pro Met Gln Gln Pro Pro Val Gly Ala Gly Gly Pro Pro Pro
545                 550                 555                 560

Met Pro Pro His Pro Gly Met Pro Gly Gly Pro Pro Gln Gln Gln Gln
                565                 570                 575

Ser Gln Gln Gln Gln Ala Ser Asn Ser Ala Ser Ser Ala Ser Asn Ser
            580                 585                 590

Pro Gln Gln Thr Pro Pro Pro Ala Pro Pro Pro Asn Gln Gly Met Asn
        595                 600                 605

Asn Met Ala Thr Pro Pro Pro Pro Pro Gln Gly Ala Ala Gly Gly Gly
    610                 615                 620

Tyr Pro Met Pro Pro His Met His Gly Gly Tyr Lys Met Gly Gly Pro
625                 630                 635                 640

Gly Gln Ser Pro Gly Ala Gln Gly Tyr Pro Pro Gln Gln Pro Gln Gln
                645                 650                 655

Tyr Pro Pro Gly Asn Tyr Pro Pro Arg Pro Gln Tyr Pro Pro Gly Ala
            660                 665                 670

Tyr Ala Thr Gly Pro Pro Pro Pro Pro Thr Ser Gln Ala Gly Ala Gly
        675                 680                 685
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Gly Ala Asn Ser Met Pro Ser Gly Ala Gln Ala Gly Gly Tyr Pro Gly
     690                 695                 700

Arg Gly Met Pro Asn His Thr Gly Gln Tyr Pro Pro Tyr Gln Trp Val
705                 710                 715                 720

Pro Pro Ser Pro Gln Gln Thr Val Pro Gly Gly Ala Pro Gly Gly Ala
                725                 730                 735

Met Val Gly Asn His Val Gln Gly Lys Gly Thr Pro Pro Pro Pro Val
            740                 745                 750

Val Gly Gly Pro Pro Pro Pro Gln Gly Ser Gly Ser Pro Arg Pro Leu
        755                 760                 765

Asn Tyr Leu Lys Gln His Leu Gln His Lys Gly Gly Tyr Gly Gly Ser
    770                 775                 780

Pro Thr Pro Pro Gln Gly Pro Gln Gly Tyr Gly Asn Gly Pro Thr Gly
785                 790                 795                 800

Met His Pro Gly Met Pro Met Gly Pro Pro His His Met Gly Pro Pro
                805                 810                 815

His Gly Pro Thr Asn Met Gly Pro Pro Thr Ser Thr Pro Pro Gln Ser
            820                 825                 830

Gln Met Leu Gln Gly Gly Gln Pro Gln Gly Gln Gly Ala Ser Gly Gly
        835                 840                 845

Pro Glu Ser Gly Gly Pro Glu His Ile Ser Gln Asp Asn Gly Ile Ser
    850                 855                 860

Ser Ser Gly Pro Thr Gly Ala Ala Gly Met His Ala Val Thr Ser Val
865                 870                 875                 880

Val Thr Thr Gly Pro Asp Gly Thr Ser Met Asp Glu Val Ser Gln Gln
                885                 890                 895

Ser Thr Leu Ser Asn Ala Ser Ala Ala Ser Gly Glu Asp Pro Gln Cys
            900                 905                 910

Thr Thr Pro Lys Ser Arg Lys Asn Asp Pro Tyr Ser Gln Ser His Leu
        915                 920                 925

Ala Pro Pro Ser Thr Ser Pro His Pro Val Val Met His Pro Gly Gly
    930                 935                 940

Gly Pro Gly Glu Glu Tyr Asp Met Ser Ser Pro Pro Asn Trp Pro Arg
945                 950                 955                 960

Pro Ala Gly Ser Pro Gln Val Phe Asn His Val Pro Val Pro Gln Glu
                965                 970                 975

Pro Phe Arg Ser Thr Ile Thr Thr Thr Lys Lys Ser Asp Ser Leu Cys
            980                 985                 990

Lys Leu Tyr Glu Met Asp Asp Asn  Pro Asp Arg Arg Gly  Trp Leu Asp
        995                 1000                1005

Lys Leu  Arg Ala Phe Met Glu  Glu Arg Arg Thr Pro  Ile Thr Ala
```

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Cys Pro Thr Ile Ser Lys Gln Pro Leu Asp Leu Tyr Arg Leu Tyr
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Ile Tyr Val Lys Glu Arg Gly Gly Phe Val Glu Val Thr Lys Ser
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Lys Thr Trp Lys Asp Ile Ala Gly Leu Leu Gly Ile Gly Ala Ser
1055 1060 1065

Ser Ser Ala Ala Tyr Thr Leu Arg Lys His Tyr Thr Lys Asn Leu
1070 1075 1080

Leu Thr Phe Glu Cys His Phe Asp Arg Gly Asp Ile Asp Pro Leu
1085 1090 1095

Pro Ile Ile Gln Gln Val Glu Ala Gly Ser Lys Lys Lys Thr Ala
1100 1105 1110

Lys Ala Ala Ser Val Pro Ser Pro Gly Ser Ser Asn Ser Gln Asp
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Ser Phe Pro Ala Pro Pro Gly Ser Ala Pro Asn Ala Ala Ile Asp
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Gly Tyr Pro Gly Tyr Pro Gly Gly Ser Pro Tyr Pro Val Ala Ser
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Gly Pro Gln Pro Asp Tyr Ala Thr Ala Gly Gln Met Gln Arg Pro
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Pro Ser Gln Asn Asn Pro Gln Thr Pro His Pro Gly Ala Ala Ala
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Ala Val Ala Ala Gly Asp Asn Ile Ser Val Ser Asn Pro Phe Glu
1190 1195 1200

Asp Pro Ile Ala Ala Gly Gly Gly Pro Gly Ser Gly Thr Gly Pro
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Gly Pro Gly Gln Gly Pro Gly Pro Gly Ala Ala Ser Gly Gly Ala
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Gly Ala Val Gly Ala Val Gly Gly Gly Pro Gln Pro His Pro Pro
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Pro Pro His Ser Pro His Thr Ala Ala Gln Gln Ala Ala Gly Gln
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His Gln Gln Gln His Pro Gln His Gln His Pro Gly Leu Pro Gly
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Pro Pro Ser Val Gly Gly Gly Pro Pro Pro Ala Pro Gln Gln His
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Pro Pro Gly Gln Pro Phe Gly Gln Gly Pro Gly Gln Tyr Pro Pro
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Gln Asn Arg Asn Met Tyr Pro Pro Tyr Gly Pro Glu Gly Glu Ala
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Pro Pro Thr Gly Ala Asn Gln Tyr Gly Pro Tyr Gly Ser Arg Pro
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Tyr Ser Gln Pro Pro Pro Gly Gly Pro Gln Pro Pro Thr Gln Thr
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Val Ala Gly Gly Pro Pro Ala Gly Gly Ala Pro Gly Ala Pro Pro
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Ser Ser Ala Tyr Pro Thr Gly Arg Pro Ser Gln Gln Asp Tyr Tyr
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Gln Pro Pro Pro Asp Gln Ser Pro Gln Pro Arg Arg His Pro Asp
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Phe Ile Lys Asp Ser Gln Pro Tyr Pro Gly Tyr Asn Ala Arg Pro
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Gln Ile Tyr Gly Ala Trp Gln Ser Gly Thr Gln Gln Tyr Arg Pro
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Gln Tyr Pro Ser Ser Pro Ala Pro Gln Asn Trp Gly Gly Ala Pro
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Pro Gln Gln Gln Gln Gln Gln Pro Pro Tyr Gln Gln Val Ala Gly
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Pro Pro Gly Gln Gln Pro Pro Gln Ala Pro Pro Gln Trp Ala Gln
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Met Asn Pro Gly Gln Thr Ala Gln Ser Gly Ile Ala Pro Pro Gly
1595 1600 1605

Ser Pro Leu Arg Pro Pro Ser Gly Pro Gly Gln Gln Asn Arg Met
1610 1615 1620

```
Pro Gly  Met Pro Ala Gln Gln  Gln Gln Ser Gln Gln  Gln Gly Gly
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Val Pro  Gln Pro Pro Pro Gln  Gln Ala Ser His Gly  Gly Val Pro
    1640                 1645                 1650

Ser Pro  Gly Leu Pro Gln Val  Gly Pro Gly Gly Met  Val Lys Pro
    1655                 1660                 1665

Pro Tyr  Ala Met Pro Pro Pro  Pro Ser Gln Gly Val  Gly Gln Gln
    1670                 1675                 1680

Val Gly  Gln Gly Pro Pro Gly  Gly Met Met Ser Gln  Lys Pro Pro
    1685                 1690                 1695

Pro Met  Pro Gly Gln Ala Met  Gln Gln Gln Pro Leu  Gln Gln Gln
    1700                 1705                 1710

Pro Pro  Ser His Gln His Pro  His Pro His Gln His  Pro Gln His
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Gln His  Pro His Gln Met Pro  Pro Asn Gln Thr Ala  Pro Gly Gly
    1730                 1735                 1740

Tyr Gly  Pro Pro Gly Met Pro  Gly Gly Gly Ala Gln  Leu Val Lys
    1745                 1750                 1755

Lys Glu  Leu Ile Phe Pro His  Asp Ser Val Glu Ser  Thr Thr Pro
    1760                 1765                 1770

Val Leu  Tyr Arg Arg Lys Arg  Leu Met Lys Ala Asp  Val Cys Pro
    1775                 1780                 1785

Val Asp  Pro Trp Arg Ile Phe  Met Ala Met Arg Ser  Gly Leu Leu
    1790                 1795                 1800

Thr Glu  Cys Thr Trp Ala Leu  Asp Val Leu Asn Val  Leu Leu Phe
    1805                 1810                 1815

Asp Asp  Ser Thr Val Gln Phe  Phe Gly Ile Ser Asn  Leu Pro Gly
    1820                 1825                 1830

Leu Leu  Thr Leu Leu Leu Glu  His Phe Gln Lys Asn  Leu Ala Glu
    1835                 1840                 1845

Met Phe  Asp Glu Arg Glu Asn  Glu Glu Gln Ser Ala  Leu Leu Ala
    1850                 1855                 1860

Glu Asp  Ala Asp Asp Asp Ala  Asp Ser Gly Thr Val  Met Cys Glu
    1865                 1870                 1875

Lys Leu  Arg Thr Ser Gly Arg  Gln Pro Arg Cys Val  Arg Ser Ile
    1880                 1885                 1890

Ser Ser  Tyr Asn Arg Arg Arg  His Tyr Glu Asn Met  Asp Arg Ser
    1895                 1900                 1905

Gly Lys  Asp Gly Ala Gly Asn  Gly Ser Asp Ser Glu  Asp Ala Asp
    1910                 1915                 1920

Glu Gly  Ile Asp Leu Gly Gln  Val Arg Val Gln Pro  Asn Pro Glu
```

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Glu Arg Ser Leu Leu Leu Ser Phe Thr Pro Asn Tyr Thr Met Val
1940 1945 1950

Thr Arg Lys Gly Val Pro Val Arg Ile Gln Pro Ala Glu Asn Asp
1955 1960 1965

Ile Phe Val Asp Glu Arg Gln Lys Ala Trp Asp Ile Asp Thr Asn
1970 1975 1980

Arg Leu Tyr Glu Gln Leu Glu Pro Val Gly Ser Asp Ala Trp Thr
1985 1990 1995

Tyr Gly Phe Thr Glu Pro Asp Pro Leu Asp Gly Ile Ile Asp Val
2000 2005 2010

Phe Lys Ser Glu Ile Val Asn Ile Pro Phe Ala Arg Tyr Ile Arg
2015 2020 2025

Ser Asp Lys Lys Gly Arg Lys Arg Thr Glu Leu Ala Ser Ser Ser
2030 2035 2040

Arg Lys Pro Glu Ile Lys Thr Glu Glu Asn Ser Thr Glu Glu Gln
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Thr Phe Asn Lys Lys Arg Arg Leu Val Ser Gly Gly Ser Ser Ser
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Ser Gly Ala His Ala Glu Gly Lys Lys Ser Lys Leu Thr Ser Glu
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Glu Phe Ala Gln Pro Asn Ala Glu Val Lys Lys Glu Pro Gly Thr
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Ala Asp Ser Asp Cys Arg Pro Val Asp Met Asp Ile Glu Ala Pro
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Gln Gln Arg Leu Thr Asn Gly Val Ala Pro Cys Ser Ser Thr Pro
2120 2125 2130

Ala Ile Phe Asp Pro Arg Thr Thr Ala Lys Asp Glu Ala Arg Val
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Leu Gln Arg Arg Arg Asp Ser Ser Phe Glu Asp Glu Cys Tyr Thr
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Arg Asp Glu Ala Ser Leu His Leu Val Ser Glu Ser Gln Asp Ser
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Leu Ala Arg Arg Cys Ile Ala Leu Ser Asn Ile Phe Arg Asn Leu
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Thr Phe Val Pro Gly Asn Glu Thr Val Leu Ala Lys Ser Thr Arg
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Phe Leu Ala Val Leu Gly Arg Leu Leu Leu Leu Asn His Glu His
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Leu Arg Arg Thr Pro Lys Thr Arg Asn Tyr Asp Arg Glu Glu Asp
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Thr Asp Phe Ser Asp Ser Cys Ser Ser Leu Gln Gly Glu Arg Glu
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Trp Trp Trp Asp Tyr Leu Ile Thr Ile Arg Glu Asn Met Leu Val
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Ala Met Ala Asn Ile Ala Gly His Leu Glu Leu Ser Arg Tyr Asp
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Glu Leu Ile Ala Arg Pro Leu Ile Asp Gly Leu Leu His Trp Ala
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Val Cys Pro Ser Ala His Gly Gln Asp Pro Phe Pro Ser Cys Gly
2300 2305 2310

Pro Asn Ser Val Leu Ser Pro Gln Arg Leu Ala Leu Glu Ala Leu
2315 2320 2325

Cys Lys Leu Cys Val Thr Asp Ala Asn Val Asp Leu Val Ile Ala
2330 2335 2340

Thr Pro Pro Phe Ser Arg Leu Glu Lys Leu Cys Ala Val Leu Thr
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Arg His Leu Cys Arg Asn Glu Asp Gln Val Leu Arg Glu Phe Ser
2360 2365 2370

Val Asn Leu Leu His Tyr Leu Ala Ala Ala Asp Ser Ala Met Ala
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Arg Thr Val Ala Leu Gln Ser Pro Cys Ile Ser Tyr Leu Val Ala
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Phe Ile Glu Gln Ala Glu Gln Thr Ala Leu Gly Val Ala Asn Gln
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His Gly Ile Asn Tyr Leu Arg Glu Asn Pro Asp Ser Met Gly Thr
2420 2425 2430

Ser Leu Asp Met Leu Arg Arg Ala Ala Gly Thr Leu Leu His Leu
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Ala Lys His Pro Asp Asn Arg Ser Leu Phe Met Gln Gln Glu Gln
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Arg Leu Leu Gly Leu Val Met Ser His Ile Leu Asp Gln Gln Val
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Ala Leu Ile Ile Ser Arg Val Leu Tyr Gln Val Ser Arg Gly Thr
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Gly Pro Ile His Ser Val Glu Phe Arg Leu Leu Gln Gln Arg Gln
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Ala Gly Gly Ser Ala Thr Val Lys Ala Glu Thr Ala Ser Thr Glu
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Ala Ala Thr Phe Asn Asp Val Ser Asn Ser Ser Thr Asn Ser Asn
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Ser Cys Gly Thr Ala Ser Ser Asn Gln Thr Asn Asn Ser Thr Thr
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Asn Ser Ser His Ser Ser Ser Ala Ile Ser Ser Gln Ser Ala Ile
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Thr Val Ala Ala Pro Ser Ala Ala Ala Thr Gly Ala Gly Ser Ala
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ctgcccacat atctgctgaa catttgtgag gtgtgcggca gctctcagtg tccgtactgc 5160

tccatctaca acatgggctg gcgcgcctcc atgtccatgt ccctgctctt cttcagcgta 5220

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<211> 1760
<212> PRT
<213> Drosophila melanogaster

<400> 38

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Asp Ala Leu Gln Pro Ala Val Gly Gln Asn Asp Asn Tyr Tyr Asn Pro
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Asn Gln Asn Gln Gln Asn Pro Gln Gln Pro Leu Leu Pro Asn Gln Gln
35 40 45

Trp Gly Asn Asn Pro Gln Thr Asn Gln Tyr Ser Asn Asn Asn Gln Asn
50 55 60

Phe Gly Gln Thr Asn Pro Ser Asp Arg Pro Pro Tyr Arg Thr Asp Ser
65 70 75 80

Gly Ser Tyr Asn Asp Ile Ala Gly Gln Asp Asp Tyr Asn Lys Arg Val
85 90 95

Gly Gly Gly Tyr Gln Asp Asn Glu Glu Pro Ser Leu Thr Arg Gly Lys

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            100                 105                 110

Ser Ser Tyr Asn Ile Lys Ala Thr Phe Leu Glu Ser Leu His Ser Arg
        115                 120                 125

Glu Pro Thr Tyr Phe Ile Val Ala Ser Arg Met Val Arg Pro Gly Leu
    130                 135                 140

Ile Tyr Gln Val Ser Val Ser Ile Leu Gln Ala Gln Tyr Pro Ile Thr
145                 150                 155                 160

Val His Ala Ser Ile Ala Cys Asp Gly Val Gln Ile Ser Gly Asp Ser
                165                 170                 175

Lys Asp Val Lys Glu Gly Ile Pro Glu Thr Leu Leu Met Arg Ile Pro
            180                 185                 190

Pro Thr Ser Val Thr Gly Ser Tyr Lys Leu Arg Val Glu Gly Phe Tyr
        195                 200                 205

Gln Asn Val Phe Gly Gly Leu Ala Phe Leu Asn Glu Thr Arg Leu Asp
    210                 215                 220

Phe Ser Gln Arg Ser Met Thr Ile Phe Val Gln Thr Asp Lys Pro Leu
225                 230                 235                 240

Tyr Met Gln Gly Glu Thr Val Arg Phe Arg Thr Ile Pro Ile Thr Thr
                245                 250                 255

Glu Leu Lys Gly Phe Asp Asn Pro Val Asp Val Tyr Met Leu Asp Pro
            260                 265                 270

Asn Arg His Ile Leu Lys Arg Trp Leu Ser Arg Gln Ser Asn Leu Gly
        275                 280                 285

Ser Val Ser Leu Glu Tyr Lys Leu Ser Asp Gln Pro Thr Phe Gly Glu
    290                 295                 300

Trp Thr Ile Arg Val Ile Ala Gln Gly Gln Gln Glu Glu Ser His Phe
305                 310                 315                 320

Thr Val Glu Glu Tyr Tyr Gln Thr Arg Phe Glu Val Asn Val Thr Met
                325                 330                 335

Pro Ala Tyr Phe Phe Thr Thr Asp Pro Phe Ile Tyr Gly Arg Val Met
            340                 345                 350

Ala Asn Phe Thr Ser Gly Leu Pro Val Arg Gly Asn Leu Thr Ile Lys
        355                 360                 365

Ala Thr Ile Arg Pro Ile Gly Tyr Phe Ser Asn Gln Val Leu Asn Glu
    370                 375                 380

Lys Tyr Arg Leu Gly Arg Ser Pro Leu Glu Gln Thr Asn Leu Tyr Asn
385                 390                 395                 400

Glu Arg Trp Arg Tyr Asn Asn Pro Asn Gln Asn Pro Gln Val Gln Tyr
                405                 410                 415

Asn Val Pro Gly Gln Leu Pro Gln Asp Gly Ala Asp Leu Ser Gln Asp
            420                 425                 430
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Ile Leu Tyr Arg Asn Gln Tyr Val Val Glu Arg His Tyr Gln Phe Asp
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Glu Glu Trp Pro Phe Trp Val Arg Lys Pro Glu Tyr Gln Asp Ser Ser
450 455 460

Tyr Glu Ala Trp Ser Gly Thr Tyr Arg Lys Thr Leu Pro Tyr Leu Arg
465 470 475 480

Tyr Phe Asn Gly Thr Phe Asp Phe Lys Trp Pro Leu Arg Glu Leu Glu
485 490 495

Leu Leu Val Pro Asn Leu Ala Asn Ser Glu Val Leu Ile Thr Ala Thr
500 505 510

Val Gly Glu Lys Phe Tyr Asp Glu Ile Ile Ser Gly Tyr Ser Val Ala
515 520 525

Arg Val Tyr Asn Ser Ser Leu Arg Val Val Phe Leu Gly Asp Ser Pro
530 535 540

Gln Val Phe Lys Pro Ala Met Pro Phe Thr Thr Tyr Leu Ala Val Glu
545 550 555 560

Tyr His Asp Gly Ser Pro Ile Asp Pro Asn Leu Leu Arg Gln Gly Leu
565 570 575

Met Glu Val Ser Gly Phe Val Glu Ser Arg Asn Gly Gly Arg Arg Asp
580 585 590

Trp Pro Ala Gln Arg Leu Pro Met Ser Gln Gln Ser Asp Gly Ile Trp
595 600 605

Glu Val Lys Ile Asp Ile Arg Asn Asp Leu Asn Leu Asp Asp Arg Pro
610 615 620

Gln Ala Arg Asp Phe Leu Asn Gly Val Gln Asn Met Arg Leu Gln Ala
625 630 635 640

Asn Phe Val Asp Pro Arg Gly Glu Arg Ile Gln Thr Glu Leu Leu Leu
645 650 655

Val Ser His Tyr Ser Pro Arg Asn Gln His Ile Lys Val Thr Thr Ser
660 665 670

Thr Glu Lys Pro Val Val Gly Glu Tyr Ile Ile Phe His Ile Arg Thr
675 680 685

Asn Phe Tyr Leu Glu Glu Phe Asn Tyr Leu Ile Met Ser Lys Gly Val
690 695 700

Ile Leu Val Asn Asp Arg Glu Thr Ile Thr Glu Gly Ile Lys Thr Ile
705 710 715 720

Ala Val Val Leu Ser Ser Glu Met Ala Pro Val Ala Thr Ile Val Val
725 730 735

Trp Lys Ile Asn Gln Gln Gly Gln Val Val Ala Asp Ser Leu Thr Phe
740 745 750

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Pro Val Asn Gly Ile Ser Arg Asn Asn Phe Thr Val Tyr Ile Asn Asn
        755                 760                 765

Arg Lys Ala Arg Thr Gly Glu Lys Val Glu Val Ala Ile Phe Gly Glu
    770                 775                 780

Pro Gly Ser Tyr Val Gly Leu Ser Gly Ile Asp Ser Ala Phe Tyr Thr
785                 790                 795                 800

Met Gln Ala Gly Asn Glu Leu Thr Tyr Ala Lys Ile Ile Thr Lys Met
                805                 810                 815

Ser Asn Phe Asp Glu Gln Thr Asn Gly Thr Tyr Lys His Ile Trp Tyr
            820                 825                 830

Ser His Glu Gly Asn Pro Asp Glu Leu Val Tyr Phe Pro Ala Ser Ser
        835                 840                 845

Phe Gly Val Asp Ala Asn Arg Thr Phe Glu Tyr Ser Gly Leu Ile Val
    850                 855                 860

Phe Thr Asp Gly Tyr Val Pro Arg Arg Gln Asp Thr Cys Asn Arg Thr
865                 870                 875                 880

Leu Gly Phe Gly Glu Cys Leu Ser Gly Arg Cys Tyr Arg Leu Glu Lys
                885                 890                 895

Gln Cys Asp Gly Leu Phe Asp Cys Asp Asp Gly Thr Asp Glu Ile Asn
            900                 905                 910

Cys His Ala Arg Asn Asp Thr Glu Leu Leu Asn Tyr Arg Lys Tyr Arg
        915                 920                 925

Phe Asn Arg Val Leu Arg His Tyr Glu Asn Val Trp Leu Trp Lys Asp
    930                 935                 940

Val Asn Ile Gly Pro His Gly Arg Tyr Ile Phe Asn Val Glu Val Pro
945                 950                 955                 960

Asp Arg Pro Ala Tyr Trp Met Val Ser Ala Phe Ser Val Ser Pro Ser
                965                 970                 975

Lys Gly Phe Gly Met Met Asn Lys Ala Leu Glu Tyr Val Gly Val Gln
            980                 985                 990

Pro Phe Phe Ile Asn Val Glu Met  Pro Glu Ala Cys Arg  Gln Gly Glu
        995                 1000                1005

Gln Val  Gly Ile Arg Val Thr  Val Phe Asn Tyr Met  Ile Thr Pro
    1010                1015                1020

Ile Glu  Ala Ile Val Val Leu  His Asp Ser Pro Asp  Tyr Lys Phe
    1025                1030                1035

Val His  Val Glu Glu Asp Gly  Ile Val Arg Ser Tyr  Asn Pro Arg
    1040                1045                1050

Thr Ser  Phe Gly Glu His Gln  Phe Phe Ile Tyr Leu  Glu Ala Gln
    1055                1060                1065

Gly Thr  Thr Val Val Tyr Val  Pro Val Val Pro Gln  Arg Leu Gly
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Asn Val Asp Val Thr Leu His Val Ala Thr Leu Leu Gly Thr Asp
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Thr Ile Thr Arg Thr Leu His Val Glu Ser Asp Gly Leu Pro Gln
1100 1105 1110

Tyr Arg His Gln Ser Val Leu Leu Asp Leu Ser Asn Arg Ala Tyr
1115 1120 1125

Val Leu Glu Tyr Met His Val Asn Val Thr Gln Thr Pro Glu Ile
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Pro Tyr Gln Val Asp Arg Tyr Phe Val Tyr Gly Ser Asn Lys Ala
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Arg Ile Ser Val Val Gly Asp Val Val Gly Pro Ile Phe Pro Thr
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Met Pro Val Asn Ala Ser Ser Leu Leu Ser Leu Pro Met Glu Ser
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Gly Glu Gln Asn Ala Phe Ser Phe Ala Ala Asn Leu Tyr Thr Ile
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Met Tyr Met Arg Leu Ile Asn Gln Arg Asn Lys Thr Leu Glu Lys
1205 1210 1215

Asn Ala Phe Tyr His Met Asn Ile Gly Tyr Gln Arg Gln Leu Ser
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Phe Met Arg Pro Asp Gly Ser Phe Ser Leu Phe Arg Ser Asp Trp
1235 1240 1245

Asn Asn Ser Asp Ser Ser Val Trp Leu Thr Ser Tyr Cys Leu Arg
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Val Phe Gln Glu Ala Ser Phe Tyr Glu Trp Glu Asn Phe Ile Trp
1265 1270 1275

Ile Asp Ala Thr Ile Ile Glu Lys Asn Met Arg Trp Leu Leu Gln
1280 1285 1290

His Gln Thr Pro Gln Gly Ser Phe Phe Glu Val Thr Trp Leu Pro
1295 1300 1305

Asp Arg Lys Met Asn Arg Thr Asn Phe Asp Lys Asn Ile Thr Leu
1310 1315 1320

Thr Ser His Val Leu Ile Thr Leu Ala Thr Val Lys Asp Ile Ser
1325 1330 1335

Gly Thr Leu Gly Ser Arg Val Ala Leu Ala Thr Gln Arg Ala Leu
1340 1345 1350

Ala Tyr Ile Glu Arg Asn Met Asp Phe Leu Arg His Gln Ala Gln
1355 1360 1365

Pro Phe Asp Val Ala Ile Thr Ala Tyr Ala Leu Gln Leu Cys Asn
1370 1375 1380

Ser Pro Ile Ala Glu Glu Val Phe Ala Ile Leu Arg Arg Gln Ala
1385 1390 1395

Arg Thr Ile Gly Asp Phe Met Tyr Trp Gly Asn Gln Glu Ile Pro
1400 1405 1410

Gln Pro Pro Arg Lys Leu Glu Asn Gln Lys Trp Phe Ser Leu Pro
1415 1420 1425

Arg Leu Pro Tyr Glu Tyr Asp Ser Leu Asn Ile Glu Thr Thr Ala
1430 1435 1440

Tyr Ala Leu Leu Val Tyr Val Ala Arg Arg Glu Phe Phe Val Asp
1445 1450 1455

Pro Ile Val Arg Trp Leu Asn Ser Gln Arg Leu Asn Asp Gly Gly
1460 1465 1470

Trp Ala Ser Thr Gln Asp Thr Ser Ala Ala Leu Lys Ala Leu Val
1475 1480 1485

Glu Tyr Thr Val Arg Ser Arg Leu Arg Glu Val Ser Ser Leu Thr
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Val Glu Ile Glu Ala Ser Ser Gln Gly Gly Lys Thr Gln Thr Leu
1505 1510 1515

Tyr Ile Asp Asp Thr Asn Leu Ala Lys Leu Gln Ser Ile Glu Ile
1520 1525 1530

Pro Asp Ala Trp Gly Thr Ile Lys Val Gln Ala Lys Gly Ala Gly
1535 1540 1545

Tyr Ala Ile Leu Gln Met His Val Gln Tyr Asn Val Asp Ile Glu
1550 1555 1560

Lys Phe Gln Thr Lys Pro Pro Val Pro Ala Phe Gly Leu His Thr
1565 1570 1575

Lys Ala Ile Phe His Gly Arg Asn Gln Ser His Ile Ser Tyr Val
1580 1585 1590

Ala Cys Gln Asn Trp Ile Asn Gln Asn Glu Ser Glu Arg Ser Gly
1595 1600 1605

Met Ala Val Leu Asp Val Ala Ile Pro Thr Gly Tyr Trp Ile Gln
1610 1615 1620

Gln Gln Lys Leu Asp Thr Tyr Val Leu Ser Asn Arg Val Arg Asn
1625 1630 1635

Leu Arg Arg Ala Arg Tyr Leu Glu Arg Lys Ile Val Phe Tyr Phe
1640 1645 1650

Asp Tyr Leu Asp His Glu Asp Ile Cys Val Asn Phe Thr Ile Glu
1655 1660 1665

Arg Trp Tyr Pro Val Ala Asn Met Ser Arg Tyr Leu Pro Val Arg
1670 1675 1680

Ile Tyr Asp Tyr Tyr Ala Pro Glu Arg Phe Asn Glu Ser Ile Phe
1685 1690 1695

Asp Ala Leu Pro Thr Tyr Leu Leu Asn Ile Cys Glu Val Cys Gly
1700 1705 1710

Ser Ser Gln Cys Pro Tyr Cys Ser Ile Tyr Asn Met Gly Trp Arg
1715 1720 1725

Ala Ser Met Ser Met Ser Leu Leu Phe Phe Ser Val Phe Ile Tyr
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Leu Leu Arg Ser Arg Thr His Leu Val Leu Asn Met Met Gln Leu
1745 1750 1755

Leu Thr
1760

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<211> 1659
<212> DNA
<213> Drosophila melanogaster

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ggtttcatca cctccatgac ggaacacttt tgtggtacct gcaatagatt gcgactcact 960

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<212> PRT
<213> Drosophila melanogaster

<400> 40

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Ala Thr Thr Gly Tyr Leu Asn Leu Ala Thr Ala Ser Val Gln Pro Leu
35 40 45

Glu Pro Glu Lys Gln Val Leu Arg Lys Asn Ser Pro Leu Thr Asp Ser
50 55 60

Phe Gly Arg His His Thr Tyr Leu Arg Ile Ser Leu Thr Glu Arg Cys
65 70 75 80

Asn Leu Arg Cys Asp Tyr Cys Met Pro Ala Glu Gly Val Pro Leu Gln
85 90 95

Pro Lys Asn Lys Leu Leu Thr Thr Glu Glu Ile Leu Arg Leu Ala Arg
100 105 110

Ile Phe Val Glu Gln Gly Val Arg Lys Ile Arg Leu Thr Gly Gly Glu
115 120 125

Pro Thr Val Arg Arg Asp Ile Val Glu Ile Val Ala Gln Met Lys Ala
130 135 140

Leu Pro Glu Leu Glu Gln Ile Gly Ile Thr Thr Asn Gly Leu Val Leu
145 150 155 160

Thr Arg Leu Leu Leu Pro Leu Gln Arg Ala Gly Leu Asp Asn Leu Asn
165 170 175

Ile Ser Leu Asp Thr Leu Lys Arg Asp Arg Phe Glu Lys Ile Thr Arg

180 185 190

Arg Lys Gly Trp Glu Arg Val Ile Ala Gly Ile Asp Leu Ala Val Gln
195 200 205

Leu Gly Tyr Arg Pro Lys Val Asn Cys Val Leu Met Arg Asp Phe Asn
210 215 220

Glu Asp Glu Ile Cys Asp Phe Val Glu Phe Thr Arg Asn Arg Pro Val
225 230 235 240

Asp Val Arg Phe Ile Glu Tyr Met Pro Phe Ser Gly Asn Lys Trp His
245 250 255

Thr Glu Arg Leu Ile Ser Tyr Lys Asp Thr Leu Gln Ile Ile Arg Gln
260 265 270

Arg Trp Pro Asp Phe Lys Ala Leu Pro Asn Gly Pro Asn Asp Thr Ser
275 280 285

Lys Ala Tyr Ala Val Pro Gly Phe Lys Gly Gln Val Gly Phe Ile Thr
290 295 300

Ser Met Thr Glu His Phe Cys Gly Thr Cys Asn Arg Leu Arg Leu Thr
305 310 315 320

Ala Asp Gly Asn Ile Lys Val Cys Leu Phe Gly Asn Lys Glu Phe Ser
325 330 335

Leu Arg Asp Ala Met Arg Asp Glu Ser Val Ser Glu Glu Gln Leu Val
340 345 350

Asp Leu Ile Gly Ala Ala Val Gln Arg Lys Lys Lys Gln His Ala Gly
355 360 365

Met Leu Asn Leu Ser Gln Met Glu Asn Arg Pro Met Ile Leu Ile Gly
370 375 380

Gly Tyr Gln Leu Thr His Val Asp Gly Gln Gly Lys Ala Gln Met Val
385 390 395 400

Asp Val Gly Ala Lys Pro Ser Thr Thr Arg Leu Ala Arg Ala Glu Ala
405 410 415

Thr Val Gln Val Gly Glu Lys Leu Thr Gln Leu Ile Ala Asp Asn Gln
420 425 430

Val Ala Lys Gly Asp Val Leu Thr Val Ala Gln Ile Ala Gly Ile Met
435 440 445

Gly Ala Lys Arg Thr Ala Glu Leu Ile Pro Leu Cys His Asn Ile Ser
450 455 460

Leu Ser Ser Val Lys Val Gln Ala Thr Leu Leu Lys Thr Glu Gln Ser
465 470 475 480

Val Arg Leu Glu Ala Thr Val Arg Cys Ser Gly Gln Thr Gly Val Glu
485 490 495

Met Glu Ala Leu Thr Ala Val Ser Val Ala Ala Leu Thr Val Tyr Asp
500 505 510

Met Cys Lys Ala Val Ser His Asp Ile Cys Ile Thr Asn Val Arg Leu
515 520 525

Leu Ser Lys Ser Gly Gly Lys Arg Asp Phe Gln Arg Glu Glu Pro Gln
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Asn Gly Ile Val Thr Glu Val Glu
545 550

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<211> 3459
<212> DNA
<213> Drosophila melanogaster

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gtggacggga ccgaagacgt ggaggaaaac gaagtggaga acgacgacga agactcacag 360

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aacggagatg gagatcacga gccagaggac gaagacgatg cccaaaagat cggtagcaca 480

gcggaaaaca gctgcgaggc cgaagatccc ctgggagcag tcacagttcc tgacgatgaa 540

ctggccagcg ggaagaaagc gcacctagat ggcgaggaga gcgtagctag cgaaggggtc 600

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gagaacggcc aagccagcat agcagaggcc agggcggcaa tagctccctc cgatggtggt 720

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<211> 1152
<212> PRT
<213> Drosophila melanogaster

<400> 42

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Ala Asp Asp Val Glu Gln Gln Val Thr Thr Val Glu Asp Asp Glu Glu
35 40 45

Gln Val Val Glu Glu Gln Gln Glu Glu Asp Val His Leu Pro Glu Ala
50 55 60

Pro Ser Asn Glu Lys Leu Glu Leu Leu Ser Ala Gly Gly Lys Asp Ile
65 70 75 80

Ser Lys Glu Asp Val Ala Gln Ala Ser Pro Gln Ala Pro Val Ala Asp
85 90 95

Glu Ile Met Glu Val Asp Gly Thr Glu Asp Val Glu Glu Asn Glu Val
100 105 110

Glu Asn Asp Asp Glu Asp Ser Gln Ile Thr Ser Ser Ser Ser Lys Glu
115 120 125

Pro Lys Leu Asp Glu Glu Asp Glu Glu Ala Thr Thr Asn Gly Asp Gly
130 135 140

Asp His Glu Pro Glu Asp Glu Asp Asp Ala Gln Lys Ile Gly Ser Thr
145 150 155 160

Ala Glu Asn Ser Cys Glu Ala Glu Asp Pro Leu Gly Ala Val Thr Val
165 170 175

Pro Asp Asp Glu Leu Ala Ser Gly Lys Lys Ala His Leu Asp Gly Glu
180 185 190

Glu Ser Val Ala Ser Glu Gly Val Val Glu Glu Glu Pro Pro Ala Lys
195 200 205

Gln Glu Asn Gly Phe Gly Ala Ser Pro Asn Gln Lys Glu Asn Gly Gln
210 215 220

Ala Ser Ile Ala Glu Ala Arg Ala Ala Ile Ala Pro Ser Asp Gly Gly

225 230 235 240

Val Val Asn Leu Asp Glu Asp Ser Asp Glu Glu Met Glu Asp Ile Thr
245 250 255

Glu His Lys Glu Pro Ala Lys Pro Thr Glu Lys Ala Ala Lys Pro Ala
260 265 270

Ser Ser Ser Gly Gly Glu Ser Ser Asp Asp Ala Val Leu Ile Ala Ser
275 280 285

Asp Ser Asp Thr Glu Ser Ala Ala Pro Pro Pro Pro Val Lys Lys Leu
290 295 300

Pro Pro Val Val Lys Ala Ile Pro Pro Pro Pro Val Gln Asp Asp Glu
305 310 315 320

Asp Asp Asp Asp Asp Asp Asp Cys Val Val Ile Glu Asp Asp Thr Pro
325 330 335

Leu Ser Ile Ser Pro Ser Gly Lys Arg Lys Ser Asp Leu Asp Asp Leu
340 345 350

Gln Leu Gln Gln Pro Ser His Lys Arg Gln Arg Ser Ser Thr Pro Ser
355 360 365

Gly Met Gly Gln Leu Thr Ile Lys Asp Ala Arg Ser Leu Met Pro Leu
370 375 380

Asp Gly Ser Pro Ser Ser Val Ser Gly Pro Arg Asp Ser Ile Tyr Pro
385 390 395 400

Val Thr Ile Thr Asn Ala Val Thr Gly Ala Ala Thr Asn Leu Gly Val
405 410 415

Val Pro Pro Lys Leu Val Pro Met Ala Gly Gly Met Ser Ala Ser Pro
420 425 430

Val Gln Leu Asn Pro Pro Thr Leu Ser Leu Thr Gly Leu Pro Ser Met
435 440 445

Thr Asn Asn Ala Asn Leu Leu Pro Gly Leu Thr Asp Asp Met Phe Val
450 455 460

Leu Glu Ala Pro Ser Phe Ile Val Pro Tyr Ile Tyr Glu Lys Pro Pro
465 470 475 480

Arg Glu Asn Ile Cys Glu Val Val Lys Ala Ile Glu Thr Lys Tyr Ala
485 490 495

Leu Ser Ala Glu Asp Leu Ala Glu Ala Asp Lys Gly Asp Glu Phe Asp
500 505 510

Met Met Thr Glu Gln Asn Lys Glu Asp Lys Pro Ala Asp Gln Ala Asp
515 520 525

Glu Ser Gly Lys Lys Lys Lys Lys Lys Arg Gly Asp Asp Glu Ser Trp
530 535 540

Ser Glu Gln Ser Asp Asp Asp Asp Asp Glu Asp Asp Asp Asp Asp Ser
545 550 555 560

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Glu Ser Gly Val Arg Thr Lys Val Leu Ile Lys Glu Ala Asn Asp Asp
                565                 570                 575

Leu Ser Ala Leu Lys Val Ala Ile Lys Pro Ala Ala Ala Leu Ala Thr
            580                 585                 590

Ala Gly Gly Val Ser Val Asn Asn Pro Gly Gly Asn Lys Pro Gly Gln
        595                 600                 605

Glu Asn Tyr Phe Glu Ser Pro Leu Gly Lys Phe Phe Met Asp Ile Gly
    610                 615                 620

Val Gly Leu Val Gln Glu Tyr Val Gln Ser Asp Leu Leu Arg Leu Gln
625                 630                 635                 640

Lys Arg Lys Met Arg Lys Ala Gln Val Gln Asn Ser Lys Glu Phe Glu
                645                 650                 655

Met Ala Ile Asn Ala Leu Ser Gly Asn Leu Gln Ala Ser Lys Thr Lys
            660                 665                 670

Asn Ala Pro Phe Lys Phe Arg Met Lys Arg Cys Glu Phe Cys Asn Phe
        675                 680                 685

Lys Ser Glu Ser Ala Met Ala Met Ala Asn His Tyr Glu Thr Pro His
    690                 695                 700

Met Asn Gly Val Leu Tyr Lys Cys Asn Phe Cys Thr Phe Glu Ile Arg
705                 710                 715                 720

Asn Ala Thr Glu Ile Val Tyr His Met Glu Ala Val His Asn Ile Lys
                725                 730                 735

Ala Arg Leu Ile Lys Pro Leu Pro Tyr His Gln Cys Pro Asn Cys Gly
            740                 745                 750

Phe Glu Asp Asn Gly Lys Ala Lys Leu Ala Arg His Gln Pro Val Cys
        755                 760                 765

Ala Lys Lys Phe Arg Pro Glu Leu Asn Leu Ala Pro Pro Asn Asp Trp
    770                 775                 780

Glu Ala Pro Ala Lys Ile Pro Arg Ile Lys Pro Arg His Gly Leu Val
785                 790                 795                 800

Gly Thr Ala Thr Ala Tyr Gln Ala Met Ala Ala Gln Ala Ala Ala Gln
                805                 810                 815

Lys Ala Ala Leu Ala Asn Ile Gln Gln Gln Gln Ala Ala Ala Gln Ala
            820                 825                 830

Arg Asn Asn Leu Gln Ala Ala Ala Leu Ala Ala Gln Asn Ala Ala Lys
        835                 840                 845

Met Arg Gln Arg Ala Pro Gln Pro Pro Lys Gln Asn Ile Val Arg Asn
    850                 855                 860

Pro Ala Pro Val Arg Gly Gly Asn Ala Met Asn Ala Gly Leu Ser Leu
865                 870                 875                 880
```

```
Pro Asn Ser Tyr Gln Leu Ala Ala Gly Gln Leu Val Gln Ala Ser Lys
                885                 890                 895

Lys Pro Met Ala Gly Gln Pro Ser Ile Ser Ile Thr Pro Leu Pro Arg
            900                 905                 910

Gln Ser Ser Val Gly Ala Gly Ala Gly Ala Ser Ser Ser Lys Ala Pro
        915                 920                 925

Gln Ala Ala Ala Gly Met Lys Pro Gly Gln Ser Pro Ser Gly Asn Asn
    930                 935                 940

Lys Ala Gln Phe Val Ile Cys Glu Ile Cys Asp Gly Tyr Ile Lys Asp
945                 950                 955                 960

Leu Glu Gln Leu Arg Asn His Met Gln Trp Met His Lys Val Lys Ile
                965                 970                 975

His Pro Lys Met Ile Tyr Asn Arg Pro Pro Leu Asn Cys Gln Lys Cys
            980                 985                 990

Gln Phe Arg Phe Phe Thr Asp Gln  Gly Leu Glu Arg His  Leu Leu Gly
        995                 1000                1005

Ser His  Gly Leu Val Thr Ser  Ser Met Gln Glu Ala  Ala Asn Lys
    1010                1015                1020

Gly Lys  Asp Ala Gly Arg Cys  Pro Val Cys Gly Arg  Met Tyr Gln
    1025                1030                1035

Trp Lys  Leu Leu Asn His Val  Ser Arg Asp His His  Met Thr Leu
    1040                1045                1050

Lys Pro  Ala His Leu Ser Tyr  Lys Cys Thr Val Cys  Thr Ala Thr
    1055                1060                1065

Phe Gly  Met Tyr Lys Gln Phe  Glu Thr His Val Tyr  Thr Ala His
    1070                1075                1080

Ser Thr  Val Ala Arg Lys Ala  Met Asp Ser Lys Lys  Asn Ser Ala
    1085                1090                1095

Gln Ser  Ser Gly Ser Gly Ser  Gly Ala Gly Met Ser  Arg Ser Ser
    1100                1105                1110

Leu Gly  Ala Ala Asn Asp Ser  Leu Leu Lys Pro Leu  Lys Ile Asn
    1115                1120                1125

Asp Glu  Ile Thr Ile Ile Pro  Gln Pro Ala Ser Lys  Pro Arg Ile
    1130                1135                1140

Thr Asn  Met Glu Ser His Val  Ile Asp
    1145                1150
```

<210> 43
<211> 1920
<212> DNA
<213> Drosophila melanogaster

<400> 43
atgcggccca atttgttttc cggcgcctcg cggctcttga cttacagccg aaatggaaaa 60

cttctgactc ggggaagaag caccaaggcc acgtccagca gcttggactc acagcaccag 120

gatgcggcga ccacggaggg tggaagagcg gaatccgtag aggagtcccc ggagcagcag 180

cgaaaactac caaccagaga gccgctggcc aaaaacttct tcatcggagt ggtggacaag 240

gagctgctgg cctatccgga ggtgattcca cgggatgaga tggcccagct ggagaattcc 300

ctgctgccgc tgaagaacta ctttgtggag ccacgtgaaa cggaggagac ctcaccggag 360

accctccgcc agctgggact ctatgggcta aatgtgtcca cagattacga gggcaaaggc 420

tatggctgga gtgccagtct aatggccagt gagccggatt caacggatat caatgtaacc 480

ctgggcctgc aaacgcatcg cgtggtcgtg gatcttctga aagaggttgg aactccgttg 540

caacagcaga ggtatctcca ggacttggcc actggtaaac tgataggtac cgaggctata 600

tatgagatat ctccacccga ggaggattac tttaacacca cggcagagtt gtttcccgaa 660

tacggaaagt ggcagctcaa tggcgaaaaa tcattcgtga tctgcacacc cggcgagcgg 720

cagcttttcc tggttctggc ccaaacccaa cagccgaatg ttccgggagt tttgggacgt 780

ggcaccacca tctttctggt tgattcccag caggaaggag tgcgcctggg cgaaaagcac 840

gccacattcg gttgccggaa agcggaaatt aggcgtgtgc acttcgaagg cgttaagttg 900

ggagaggatc aggtggtggg cctaccacac gatggcaacc gctattcgga gcagctggtg 960

cgatcctccc gcttgagggg cagcttggtg ggactatcgc tggccaagaa actgctaaac 1020

gaattggccc agtacactgt gaacaccact cagtgcggag tacaactgca agacctggag 1080

ctcacccgca tccatatgtc gcgcgcgatg tgctccgttt acgcgatgga gagcatgctc 1140

tacctgaccg ccgggttgct ggatgagttc cgtgcccagg atgtgactct ggagagtgcc 1200

ataacaaagt actttaccct gcgacaggtg tacgccattg cctcccagaa tctgggagtc 1260

gtgggaccca agagtctgct cagcggtgag accacggagc tgggactacg agatgcagcg 1320

cagctgtgca cgcaaggtga atccctggac accttgggca tgttcattgc cctcaccgga 1380

ttgcagcacg cggggcaagc catgaatacg ggcgtgcgaa agtccagaaa tccactcttc 1440

aatcctggtc acatttttgg taaattcctg gacaacaaca gcatcgacaa tcccaagacc 1500

aagatgcagc tttcggagca cgtgcatccc tcccttgagg cggctgccca gtgcattgaa 1560

ctgtcggtgg cgcgtctcca aatggccgtg gagctgatgt tcaccaagca cggcaacgcg 1620

gtggtggagc gtcaaagtga aatgcagcgc ctggcggagg tgggcaccct tatctatgcc 1680

atgtgggcca gcgtggcgag ggcatcccga tcgtattgca ttggactgcc gctggcggat 1740

catgaactgc tcacggccac agcgatatgc tcggagggca gggatcgcgt ccgcaccctc 1800

tgcacggaga tctatggcgg tcattttgtg aacaacgaca acaacctggt gcgactctcc 1860

aagcaagtgg ccaagagcaa gggctacttc gctgttcatc cgctgacatt taacttctaa 1920

<210> 44
<211> 639
<212> PRT
<213> Drosophila melanogaster

<400> 44

Met Arg Pro Asn Leu Phe Ser Gly Ala Ser Arg Leu Leu Thr Tyr Ser
1 5 10 15

Arg Asn Gly Lys Leu Leu Thr Arg Gly Arg Ser Thr Lys Ala Thr Ser
20 25 30

Ser Ser Leu Asp Ser Gln His Gln Asp Ala Ala Thr Thr Glu Gly Gly
35 40 45

Arg Ala Glu Ser Val Glu Glu Ser Pro Glu Gln Gln Arg Lys Leu Pro
50 55 60

Thr Arg Glu Pro Leu Ala Lys Asn Phe Phe Ile Gly Val Val Asp Lys
65 70 75 80

Glu Leu Leu Ala Tyr Pro Glu Val Ile Pro Arg Asp Glu Met Ala Gln
85 90 95

Leu Glu Asn Ser Leu Leu Pro Leu Lys Asn Tyr Phe Val Glu Pro Arg
100 105 110

Glu Thr Glu Glu Thr Ser Pro Glu Thr Leu Arg Gln Leu Gly Leu Tyr
115 120 125

Gly Leu Asn Val Ser Thr Asp Tyr Glu Gly Lys Gly Tyr Gly Trp Ser
130 135 140

Ala Ser Leu Met Ala Ser Glu Pro Asp Ser Thr Asp Ile Asn Val Thr
145 150 155 160

Leu Gly Leu Gln Thr His Arg Val Val Val Asp Leu Leu Lys Glu Val
165 170 175

Gly Thr Pro Leu Gln Gln Gln Arg Tyr Leu Gln Asp Leu Ala Thr Gly
180 185 190

Lys Leu Ile Gly Thr Glu Ala Ile Tyr Glu Ile Ser Pro Pro Glu Glu
195 200 205

Asp Tyr Phe Asn Thr Thr Ala Glu Leu Phe Pro Glu Tyr Gly Lys Trp
210 215 220

Gln Leu Asn Gly Glu Lys Ser Phe Val Ile Cys Thr Pro Gly Glu Arg
225 230 235 240

Gln Leu Phe Leu Val Leu Ala Gln Thr Gln Gln Pro Asn Val Pro Gly
245 250 255

Val Leu Gly Arg Gly Thr Thr Ile Phe Leu Val Asp Ser Gln Gln Glu
260 265 270

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Gly Val Arg Leu Gly Glu Lys His Ala Thr Phe Gly Cys Arg Lys Ala
        275                 280                 285

Glu Ile Arg Arg Val His Phe Glu Gly Val Lys Leu Gly Glu Asp Gln
    290                 295                 300

Val Val Gly Leu Pro His Asp Gly Asn Arg Tyr Ser Glu Gln Leu Val
305                 310                 315                 320

Arg Ser Ser Arg Leu Arg Gly Ser Leu Val Gly Leu Ser Leu Ala Lys
                325                 330                 335

Lys Leu Leu Asn Glu Leu Ala Gln Tyr Thr Val Asn Thr Thr Gln Cys
            340                 345                 350

Gly Val Gln Leu Gln Asp Leu Glu Leu Thr Arg Ile His Met Ser Arg
        355                 360                 365

Ala Met Cys Ser Val Tyr Ala Met Glu Ser Met Leu Tyr Leu Thr Ala
    370                 375                 380

Gly Leu Leu Asp Glu Phe Arg Ala Gln Asp Val Thr Leu Glu Ser Ala
385                 390                 395                 400

Ile Thr Lys Tyr Phe Thr Leu Arg Gln Val Tyr Ala Ile Ala Ser Gln
                405                 410                 415

Asn Leu Gly Val Val Gly Pro Lys Ser Leu Leu Ser Gly Glu Thr Thr
            420                 425                 430

Glu Leu Gly Leu Arg Asp Ala Ala Gln Leu Cys Thr Gln Gly Glu Ser
        435                 440                 445

Leu Asp Thr Leu Gly Met Phe Ile Ala Leu Thr Gly Leu Gln His Ala
    450                 455                 460

Gly Gln Ala Met Asn Thr Gly Val Arg Lys Ser Arg Asn Pro Leu Phe
465                 470                 475                 480

Asn Pro Gly His Ile Phe Gly Lys Phe Leu Asp Asn Asn Ser Ile Asp
                485                 490                 495

Asn Pro Lys Thr Lys Met Gln Leu Ser Glu His Val His Pro Ser Leu
            500                 505                 510

Glu Ala Ala Ala Gln Cys Ile Glu Leu Ser Val Ala Arg Leu Gln Met
        515                 520                 525

Ala Val Glu Leu Met Phe Thr Lys His Gly Asn Ala Val Val Glu Arg
    530                 535                 540

Gln Ser Glu Met Gln Arg Leu Ala Glu Val Gly Thr Leu Ile Tyr Ala
545                 550                 555                 560

Met Trp Ala Ser Val Ala Arg Ala Ser Arg Ser Tyr Cys Ile Gly Leu
                565                 570                 575

Pro Leu Ala Asp His Glu Leu Leu Thr Ala Thr Ala Ile Cys Ser Glu
            580                 585                 590

Gly Arg Asp Arg Val Arg Thr Leu Cys Thr Glu Ile Tyr Gly Gly His
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595 600 605

Phe Val Asn Asn Asp Asn Asn Leu Val Arg Leu Ser Lys Gln Val Ala
610 615 620

Lys Ser Lys Gly Tyr Phe Ala Val His Pro Leu Thr Phe Asn Phe
625 630 635

<210> 45
<211> 1467
<212> DNA
<213> Drosophila melanogaster

<400> 45
atggcaccca cagcaaacac agtgctaatt accgtgccgc ggacagcaat cacatcgaat 60

aatctgccca aattgcggcc cgccccctt acggcagctc tgctgaaggt gtcggccacg 120

ccctccgcct cgcccacgcc ctcgagttcg ggatacgcat cctcgtcgaa catggatgac 180

gataacatgg ctgcatccca gcccaaggcc aagaagcgtc gcctggacca tctaacctgg 240

gaggagaaag tgcaaagaaa gaagctaaag aaccgtgtgg ccgcccagac atcgcgtgac 300

cgcaagaagg cacgcatgga ggagatggac tacgagatca aggagctgac agacagaacg 360

gaaatactac agaacaagtg cgatagcctg caggccatca acgagtcact gctggccaag 420

aaccacaagc tggactcgga gctggagctg ctgcgccaag aactcgccga actgaagcag 480

caacagcagc acaacaccag atgcatcagc caatccaacg ccagcgcagg cgctgagggc 540

tggtatacaa caggtggaca cacagtcgtc agcgcgtctg ctggcggagc agctgaagag 600

cagcaagagc ctggcctcac tctggaaagt tgtggccctc tgcctactct acaagacatg 660

cttggcgtcg acgaagagtt cgacgtcaag cgcctcgaag agctggccga aagtctgctc 720

gcagatatca cagcagacct ggaaacaggc gctggagcga gcagcccagc tgctgcccaa 780

gatgcaggca acgcagagcg attgcctgga ccaatggtgg ggcccgcagc agagcgcttg 840

gaatccgacg ggcatagagc taatggcctg aatgttgagc aggaacagga aaccgagcac 900

aaggtcagcc taaatgtgca gatgttgaag ataaatggaa acccacagca taccacagca 960

gcgccagcct cgagaacagc cacaatcaca gcgacagcgg ccgcctcgca actacaggcc 1020

actccggaca cagtgtacgg cacgtatgat gccaagacga actcgatcac catcgtgatg 1080

gacggggatg cggtgccggt gaacgaggcc gtcgaggaga tctactgtga cggcgtcagc 1140

gctggcgacg actcaacgga cgtgatcatg aagtgtccgc cgccagcgac gtctccgtca 1200

caggtctatc tcaacgtgat gaacgccgtc gacaattcgg acgacgagga aagcttcgat 1260

ccgatcgacc gattcctacg tccgcgcgtt aaggcgatct ccccgttggc caaatccccc 1320

gcattgtctc tacactcggc cacctcggac catggatacg agtccatact gggctctccc 1380

acatccgtgg ctctcactct gcccgcagat gaggacgatt tcccctggga gagcaacttt 1440

gacgagctgt ttcccagttt gatctga 1467

<210> 46
<211> 488
<212> PRT
<213> Drosophila melanogaster

<400> 46

Met Ala Pro Thr Ala Asn Thr Val Leu Ile Thr Val Pro Arg Thr Ala
1 5 10 15

Ile Thr Ser Asn Asn Leu Pro Lys Leu Arg Pro Ala Pro Leu Thr Ala
20 25 30

Ala Leu Leu Lys Val Ser Ala Thr Pro Ser Ala Ser Pro Thr Pro Ser
35 40 45

Ser Ser Gly Tyr Ala Ser Ser Ser Asn Met Asp Asp Asp Asn Met Ala
50 55 60

Ala Ser Gln Pro Lys Ala Lys Lys Arg Arg Leu Asp His Leu Thr Trp
65 70 75 80

Glu Glu Lys Val Gln Arg Lys Lys Leu Lys Asn Arg Val Ala Ala Gln
85 90 95

Thr Ser Arg Asp Arg Lys Lys Ala Arg Met Glu Glu Met Asp Tyr Glu
100 105 110

Ile Lys Glu Leu Thr Asp Arg Thr Glu Ile Leu Gln Asn Lys Cys Asp
115 120 125

Ser Leu Gln Ala Ile Asn Glu Ser Leu Leu Ala Lys Asn His Lys Leu
130 135 140

Asp Ser Glu Leu Glu Leu Leu Arg Gln Glu Leu Ala Glu Leu Lys Gln
145 150 155 160

Gln Gln Gln His Asn Thr Arg Cys Ile Ser Gln Ser Asn Ala Ser Ala
165 170 175

Gly Ala Glu Gly Trp Tyr Thr Thr Gly Gly His Thr Val Val Ser Ala
180 185 190

Ser Ala Gly Gly Ala Ala Glu Glu Gln Gln Glu Pro Gly Leu Thr Leu
195 200 205

Glu Ser Cys Gly Pro Leu Pro Thr Leu Gln Asp Met Leu Gly Val Asp
210 215 220

Glu Glu Phe Asp Val Lys Arg Leu Glu Glu Leu Ala Glu Ser Leu Leu
225 230 235 240

Ala Asp Ile Thr Ala Asp Leu Glu Thr Gly Ala Gly Ala Ser Ser Pro
245 250 255

Ala Ala Ala Gln Asp Ala Gly Asn Ala Glu Arg Leu Pro Gly Pro Met
260 265 270

Val Gly Pro Ala Ala Glu Arg Leu Glu Ser Asp Gly His Arg Ala Asn
275 280 285

Gly Leu Asn Val Glu Gln Glu Gln Glu Thr Glu His Lys Val Ser Leu
290 295 300

Asn Val Gln Met Leu Lys Ile Asn Gly Asn Pro Gln His Thr Thr Ala
305 310 315 320

Ala Pro Ala Ser Arg Thr Ala Thr Ile Thr Ala Thr Ala Ala Ala Ser
325 330 335

Gln Leu Gln Ala Thr Pro Asp Thr Val Tyr Gly Thr Tyr Asp Ala Lys
340 345 350

Thr Asn Ser Ile Thr Ile Val Met Asp Gly Asp Ala Val Pro Val Asn
355 360 365

Glu Ala Val Glu Glu Ile Tyr Cys Asp Gly Val Ser Ala Gly Asp Asp
370 375 380

Ser Thr Asp Val Ile Met Lys Cys Pro Pro Pro Ala Thr Ser Pro Ser
385 390 395 400

Gln Val Tyr Leu Asn Val Met Asn Ala Val Asp Asn Ser Asp Asp Glu
405 410 415

Glu Ser Phe Asp Pro Ile Asp Arg Phe Leu Arg Pro Arg Val Lys Ala
420 425 430

Ile Ser Pro Leu Ala Lys Ser Pro Ala Leu Ser Leu His Ser Ala Thr
435 440 445

Ser Asp His Gly Tyr Glu Ser Ile Leu Gly Ser Pro Thr Ser Val Ala
450 455 460

Leu Thr Leu Pro Ala Asp Glu Asp Asp Phe Pro Trp Glu Ser Asn Phe
465 470 475 480

Asp Glu Leu Phe Pro Ser Leu Ile
485

<210> 47
<211> 753
<212> DNA
<213> Drosophila melanogaster

<400> 47
atgagtcaca aaatcgccgc tgtgtgcctc ttgatgagct gcctgattgc cacggcttat 60

agtgccgcta aggtgccaat ttctatctac tacgagtccc tgtgcccgga cagcgccaag 120

ttcattacgg agcaggtata tccggcggtg aagggagaac tgcgcgatgt ggtggaactc 180

actttcgtgc cattcggaaa gtctcagttc gttacccagg gctccgaagt gacgttcacc 240

tgccaccacg gaccgaacga gtgctatggc aataaggtgc atgcctgcgc catcgagcac 300

attcaggcca actcctatca ggtggagtac acgcgcgagt cgctcacgat ggacttcatc 360

aactgcctaa tgaaggccgg caagaatttc ccggacaacg tctatcccgg ccagcgatgc 420

gcctcggaga accacatcaa taactgggag aacatcaaga cctgtgccaa ctccaccgag 480

ggaagcgttc tgctccggaa ggccggcgaa agcaccatgc ggctcaagga gccactcacc 540

agcgtgccca ccattctgtt caatgagcaa ttcgacaaga aggtgaatga tcgcgcccag 600

gtgaacttgg tgggcaccat ctgccaatac gtatccgccc cgcagccgcg catctgcaac 660

cagcacaacg gagcatcgac tccatctttg gccagcgtaa gcgccatcct tagctccctg 720

ctgggtcttt ggtttatccg ctccttctac taa 753

<210> 48
<211> 250
<212> PRT
<213> Drosophila melanogaster

<400> 48

Met Ser His Lys Ile Ala Ala Val Cys Leu Leu Met Ser Cys Leu Ile
1 5 10 15

Ala Thr Ala Tyr Ser Ala Ala Lys Val Pro Ile Ser Ile Tyr Tyr Glu
20 25 30

Ser Leu Cys Pro Asp Ser Ala Lys Phe Ile Thr Glu Gln Val Tyr Pro
35 40 45

Ala Val Lys Gly Glu Leu Arg Asp Val Val Glu Leu Thr Phe Val Pro
50 55 60

Phe Gly Lys Ser Gln Phe Val Thr Gln Gly Ser Glu Val Thr Phe Thr
65 70 75 80

Cys His His Gly Pro Asn Glu Cys Tyr Gly Asn Lys Val His Ala Cys
85 90 95

Ala Ile Glu His Ile Gln Ala Asn Ser Tyr Gln Val Glu Tyr Thr Arg
100 105 110

Glu Ser Leu Thr Met Asp Phe Ile Asn Cys Leu Met Lys Ala Gly Lys
115 120 125

Asn Phe Pro Asp Asn Val Tyr Pro Gly Gln Arg Cys Ala Ser Glu Asn
130 135 140

His Ile Asn Asn Trp Glu Asn Ile Lys Thr Cys Ala Asn Ser Thr Glu
145 150 155 160

Gly Ser Val Leu Leu Arg Lys Ala Gly Glu Ser Thr Met Arg Leu Lys
165 170 175

Glu Pro Leu Thr Ser Val Pro Thr Ile Leu Phe Asn Glu Gln Phe Asp
180 185 190

Lys Lys Val Asn Asp Arg Ala Gln Val Asn Leu Val Gly Thr Ile Cys
195 200 205

Gln Tyr Val Ser Ala Pro Gln Pro Arg Ile Cys Asn Gln His Asn Gly
210 215 220

Ala Ser Thr Pro Ser Leu Ala Ser Val Ser Ala Ile Leu Ser Ser Leu
225 230 235 240

Leu Gly Leu Trp Phe Ile Arg Ser Phe Tyr
245 250

<210> 49
<211> 1365
<212> DNA
<213> Drosophila melanogaster

<400> 49
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aaactggagc aggtggacaa tctgtaccag gagtttgaga ctccggagaa ggccaacaag 120

ctgctgaagc tgaagcactt tgagaaattc aatgacacca cagaggcgct ggccgctgca 180

acggcggcgg tggagggcaa ggtagccaag ccgctgaaaa agacactcaa gaagctgctc 240

gttgacgacg tgcagtcttc gctcttggtt gccgatgcca aactgggcac agccatcaag 300

gacaaactgt cggtacagtg tgtctgcaac actggcgtcc aggagctgat gcgctgtatt 360

cgccagcagg cggacagtct gcttggtggt ctgcccaagc gtgagatgac cgccatggcc 420

ctgggtcttg cccactcctt gtcgcgctac aagcttaagt tctcgcccga caagatcgac 480

acaatgattg tgcaggccca gtgcttgctg gatgacctgg acaaggagtt gaacaactac 540

atgatgcgtg cacgcgagtg gtacggttgg cactttcccg agctgggcaa gattattacc 600

gacaacattg ccttcgtgaa gaccatcaag ttggtgggca ccagggataa tatggccaca 660

agcgatctgt ccgacattct gccagaagat gtggaggaaa aggtcaagga ggcagctgag 720

atctctatgg gtaccgaaat ctccgaggag gatgtgctga acattcagtg tctgtgcgac 780

gagatcatat cgatcaacga ttaccgcacc cacttgtacg actacttgaa ggccagaatg 840

atggccatgg ctccgaattt gacagtgctc gtgggcgaca ccgtcggcgc tcgactgatt 900

gcccatgctg gctcgctgat taacctggcc aagcatccct catctactgt acaaattctg 960

ggcgccgaga aagcactctt ccgtgcgctg aagaccaaga aggatactcc aaagtacggt 1020

ttgatctatc acgcccagtt ggtgggacag gcaagccaga agaacaaggg caaaatgtcg 1080

cgttcactgg ccgccaaagc gtcgcttgcc acgcgtgttg atgcctttgg cgaagaggct 1140

acctttgagc taggagcggc tcacaaggtt aaactggagt ctcggctgcg actcctggag 1200

gagggcaacc tgcgcaaact ctccggcacc ggcaaggcca aggccaagtt cgagaagtac 1260

caggccaaga ggcgaggtgt tcacctacca accagaggcc gacaacacct tgaacgtgaa 1320

gaagaagcgc aagcactccg agtccgaaca gcagacgcct gttaa 1365

<210> 50
<211> 454
<212> PRT
<213> Drosophila melanogaster

<400> 50

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Met Phe Val Leu Tyr Glu Thr Pro Ala Gly Tyr Ala Ile Phe Lys Leu
1               5                   10                  15

Leu Asp Glu Lys Lys Leu Glu Gln Val Asp Asn Leu Tyr Gln Glu Phe
            20                  25                  30

Glu Thr Pro Glu Lys Ala Asn Lys Leu Leu Lys Leu Lys His Phe Glu
        35                  40                  45

Lys Phe Asn Asp Thr Thr Glu Ala Leu Ala Ala Ala Thr Ala Ala Val
    50                  55                  60

Glu Gly Lys Val Ala Lys Pro Leu Lys Lys Thr Leu Lys Lys Leu Leu
65                  70                  75                  80

Val Asp Asp Val Gln Ser Ser Leu Leu Val Ala Asp Ala Lys Leu Gly
                85                  90                  95

Thr Ala Ile Lys Asp Lys Leu Ser Val Gln Cys Val Cys Asn Thr Gly
            100                 105                 110

Val Gln Glu Leu Met Arg Cys Ile Arg Gln Gln Ala Asp Ser Leu Leu
        115                 120                 125

Gly Gly Leu Pro Lys Arg Glu Met Thr Ala Met Ala Leu Gly Leu Ala
    130                 135                 140

His Ser Leu Ser Arg Tyr Lys Leu Lys Phe Ser Pro Asp Lys Ile Asp
145                 150                 155                 160

Thr Met Ile Val Gln Ala Gln Cys Leu Leu Asp Asp Leu Asp Lys Glu
                165                 170                 175

Leu Asn Asn Tyr Met Met Arg Ala Arg Glu Trp Tyr Gly Trp His Phe
            180                 185                 190

Pro Glu Leu Gly Lys Ile Ile Thr Asp Asn Ile Ala Phe Val Lys Thr
        195                 200                 205

Ile Lys Leu Val Gly Thr Arg Asp Asn Met Ala Thr Ser Asp Leu Ser
    210                 215                 220

Asp Ile Leu Pro Glu Asp Val Glu Glu Lys Val Lys Glu Ala Ala Glu
225                 230                 235                 240

Ile Ser Met Gly Thr Glu Ile Ser Glu Glu Asp Val Leu Asn Ile Gln
                245                 250                 255

Cys Leu Cys Asp Glu Ile Ile Ser Ile Asn Asp Tyr Arg Thr His Leu
            260                 265                 270

Tyr Asp Tyr Leu Lys Ala Arg Met Met Ala Met Ala Pro Asn Leu Thr
        275                 280                 285
```

Val Leu Val Gly Asp Thr Val Gly Ala Arg Leu Ile Ala His Ala Gly
290 295 300

Ser Leu Ile Asn Leu Ala Lys His Pro Ser Ser Thr Val Gln Ile Leu
305 310 315 320

Gly Ala Glu Lys Ala Leu Phe Arg Ala Leu Lys Thr Lys Lys Asp Thr
325 330 335

Pro Lys Tyr Gly Leu Ile Tyr His Ala Gln Leu Val Gly Gln Ala Ser
340 345 350

Gln Lys Asn Lys Gly Lys Met Ser Arg Ser Leu Ala Ala Lys Ala Ser
355 360 365

Leu Ala Thr Arg Val Asp Ala Phe Gly Glu Glu Ala Thr Phe Glu Leu
370 375 380

Gly Ala Ala His Lys Val Lys Leu Glu Ser Arg Leu Arg Leu Leu Glu
385 390 395 400

Glu Gly Asn Leu Arg Lys Leu Ser Gly Thr Gly Lys Ala Lys Ala Lys
405 410 415

Phe Glu Lys Tyr Gln Ala Lys Arg Arg Gly Val His Leu Pro Thr Arg
420 425 430

Gly Arg Gln His Leu Glu Arg Glu Glu Glu Ala Gln Ala Leu Arg Val
435 440 445

Arg Thr Ala Asp Ala Cys
450

<210> 51
<211> 1218
<212> DNA
<213> Drosophila melanogaster

<400> 51
atgagtgtct gtgagagcaa agccgttgtg caacagcaac tgcagcagca cttgcagcaa 60

caggcagccg cagcagttgt tgcggtcgcg caacagcagc aggctcaagc ccaagcccag 120

gctcaggctc aggcacagca gcagcaacag gcgccgcagg tggtggtccc catgaccccg 180

cagcacttga ccccacagca gcagcagcag agcacacaga gcatcgccga ctatctggcc 240

cagttgctca aggaccgcaa gcaactggcc gccttcccca acgtcttcac ccacgtcgaa 300

cgcctgctgg acgaagaaat tgcacgcgtg cgcgcctcac tgttccagat caatggggtc 360

aagaaggagc cgctcactct gcccgaaccc gagggctctg tggtgacgat gaacgagaag 420

gtttatgtgc cagtccgcga gcatccagat ttcaactttg tcggtcgcat tttgggaccc 480

cgtggcatga ccgccaagca attggaacag gagaccggct gcaagattat ggtccgaggc 540

aagggttcca tgcgcgacaa gaagaaggag gacgccaacc gtggcaagcc taactgggag 600

catctgtccg atgacctgca tgtcctgata accgtcgagg acaccgagaa ccgtgccaca 660

gtgaagttgg cccaggccgt cgccgaagta cagaagttgc tcgtgccgca agccgaaggc 720

gaagatgagc taaagaaacg tcaactcatg gaattggcga ttattaatgg cacttatagg 780

gacacaacag cgaaatctgt cgcagtgtgc gatgaggagt ggcgccgcct ggttgccgcc 840

tctgatagcc gcctgctgac atccaccggc ctgcccggcc ttgccgccca gatccgtgca 900

cccgccgccg ccccgcttgg cgccccattg atcctgaatc cccggatgac cgtccccaca 960

acggcggcca gcatattgtc cgcccaggcc gctccgacag ccgccttcga ccagaccggc 1020

catggaatga tcttcgcacc gtacgattat gcgaactacg ccgccctagc cggcaatcct 1080

ctgctcacgg aatatgctga tcatagcgta ggcgccatta agcagcagcg tcgtttggcg 1140

actaaccgcg agcatcccta tcagcgagca acggtcggag tgccagccaa gccggcgggt 1200

ttcattgaga tacagtaa 1218

<210> 52
<211> 405
<212> PRT
<213> Drosophila melanogaster

<400> 52

Met Ser Val Cys Glu Ser Lys Ala Val Val Gln Gln Gln Leu Gln Gln
1 5 10 15

His Leu Gln Gln Gln Ala Ala Ala Ala Val Val Ala Val Ala Gln Gln
20 25 30

Gln Gln Ala Gln Ala Gln Ala Gln Ala Gln Ala Gln Ala Gln Gln Gln
35 40 45

Gln Gln Ala Pro Gln Val Val Val Pro Met Thr Pro Gln His Leu Thr
50 55 60

Pro Gln Gln Gln Gln Gln Ser Thr Gln Ser Ile Ala Asp Tyr Leu Ala
65 70 75 80

Gln Leu Leu Lys Asp Arg Lys Gln Leu Ala Ala Phe Pro Asn Val Phe
85 90 95

Thr His Val Glu Arg Leu Leu Asp Glu Glu Ile Ala Arg Val Arg Ala
100 105 110

Ser Leu Phe Gln Ile Asn Gly Val Lys Lys Glu Pro Leu Thr Leu Pro
115 120 125

Glu Pro Glu Gly Ser Val Val Thr Met Asn Glu Lys Val Tyr Val Pro
130 135 140

Val Arg Glu His Pro Asp Phe Asn Phe Val Gly Arg Ile Leu Gly Pro
145 150 155 160

Arg Gly Met Thr Ala Lys Gln Leu Glu Gln Glu Thr Gly Cys Lys Ile
165 170 175

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Met Val Arg Gly Lys Gly Ser Met Arg Asp Lys Lys Lys Glu Asp Ala
            180                 185                 190

Asn Arg Gly Lys Pro Asn Trp Glu His Leu Ser Asp Asp Leu His Val
        195                 200                 205

Leu Ile Thr Val Glu Asp Thr Glu Asn Arg Ala Thr Val Lys Leu Ala
    210                 215                 220

Gln Ala Val Ala Glu Val Gln Lys Leu Leu Val Pro Gln Ala Glu Gly
225                 230                 235                 240

Glu Asp Glu Leu Lys Lys Arg Gln Leu Met Glu Leu Ala Ile Ile Asn
                245                 250                 255

Gly Thr Tyr Arg Asp Thr Thr Ala Lys Ser Val Ala Val Cys Asp Glu
            260                 265                 270

Glu Trp Arg Arg Leu Val Ala Ala Ser Asp Ser Arg Leu Leu Thr Ser
        275                 280                 285

Thr Gly Leu Pro Gly Leu Ala Ala Gln Ile Arg Ala Pro Ala Ala Ala
    290                 295                 300

Pro Leu Gly Ala Pro Leu Ile Leu Asn Pro Arg Met Thr Val Pro Thr
305                 310                 315                 320

Thr Ala Ala Ser Ile Leu Ser Ala Gln Ala Ala Pro Thr Ala Ala Phe
                325                 330                 335

Asp Gln Thr Gly His Gly Met Ile Phe Ala Pro Tyr Asp Tyr Ala Asn
            340                 345                 350

Tyr Ala Ala Leu Ala Gly Asn Pro Leu Leu Thr Glu Tyr Ala Asp His
        355                 360                 365

Ser Val Gly Ala Ile Lys Gln Gln Arg Arg Leu Ala Thr Asn Arg Glu
    370                 375                 380

His Pro Tyr Gln Arg Ala Thr Val Gly Val Pro Ala Lys Pro Ala Gly
385                 390                 395                 400

Phe Ile Glu Ile Gln
                405
```

<210> 53
<211> 1290
<212> DNA
<213> Drosophila melanogaster

<400> 53

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atgagtggca agcaggtagt catccttctg ggcagtgtcc tgatcctggg atgcttacaa     60

gtggcagcgg caacggaaac ggataacaaa accaacgatt tcgtggccac cgacgaatgg    120

cagacgattg cggaaggtca agctattcca aggggcctgc acgtgcgcat caacctacaa    180

acggggctca aggaagccaa actcttagac gaaagcgaac gtggcacgtc gctgcagagt    240

caaccggatg atcagaatgc tcgggaatct cacgatgaca acgaacccct ggctctggac    300
```

tataaaccgg acataatcga ggagtctata cggcgggtca aggagcagaa gaagagctat 360

gccgagctac gcaaagcgta caaagagttc cagaagaact ttcgcaccga cggagaactg 420

atcgtccagt taatcgatca gtttcggaac ttcagcagaa cgccgctaga gtcagagatg 480

cgctccaagc tggactgcct ggaaaatctg gagtatttgc tccatcagat agacaatgcc 540

ttgatgttca ttgataatgg gggattggat gatgtactac tgcccattgt tgtgaacgat 600

accagtacat ccctgagagt gtcggccatg cgtgtgttgg gctcgctggc gagcaacaat 660

cccaaggccc agatcaaggt gttcgaaaag aatttcgggt ctcatctggc tcagattctg 720

accagttccg gaaatgtcgg tgagatctcc gctgcattgc acgcctttgg agccttgttg 780

cggaaatttc cgctagccca gcagcgagtg ctttccacct cgggtacaca ggctctgatc 840

aaggtgctcc agagtccgga tgtggagctg cggagcaagg cgaaggtagt gactctcata 900

agcgacctag tgctggagaa gcggtcagtg ctggatgtca gcaaagatga tcccgaagcc 960

tcatccacaa tggcgcaata tgtgctcttg gacttcgagt cgtggctgaa aacgccgggc 1020

tactgcgcgg cggtggacac tgtgctaacc aaggagttcc tgctcctcct agagcaaccg 1080

gaggtggtgg aacagtttgc caccgcattg gagaccaccg aagatatgtg caccagcacg 1140

tggtcgcaaa gttccggtct caggcatgca ctattaaccg ttcgcaatcg gtatgccaac 1200

agcacggacg agtaccgact ggaggtgtcc cagattttgg ccaaactgtg cgagagattg 1260

ttcaacaagc ccaagcacac cgaactgtaa 1290

<210> 54
<211> 429
<212> PRT
<213> Drosophila melanogaster

<400> 54

Met Ser Gly Lys Gln Val Val Ile Leu Leu Gly Ser Val Leu Ile Leu
1 5 10 15

Gly Cys Leu Gln Val Ala Ala Ala Thr Glu Thr Asp Asn Lys Thr Asn
20 25 30

Asp Phe Val Ala Thr Asp Glu Trp Gln Thr Ile Ala Glu Gly Gln Ala
35 40 45

Ile Pro Arg Gly Leu His Val Arg Ile Asn Leu Gln Thr Gly Leu Lys
50 55 60

Glu Ala Lys Leu Leu Asp Glu Ser Glu Arg Gly Thr Ser Leu Gln Ser
65 70 75 80

Gln Pro Asp Asp Gln Asn Ala Arg Glu Ser His Asp Asp Asn Glu Pro
85 90 95

```
Leu Ala Leu Asp Tyr Lys Pro Asp Ile Ile Glu Glu Ser Ile Arg Arg
            100                 105                 110

Val Lys Glu Gln Lys Lys Ser Tyr Ala Glu Leu Arg Lys Ala Tyr Lys
        115                 120                 125

Glu Phe Gln Lys Asn Phe Arg Thr Asp Gly Glu Leu Ile Val Gln Leu
    130                 135                 140

Ile Asp Gln Phe Arg Asn Phe Ser Arg Thr Pro Leu Glu Ser Glu Met
145                 150                 155                 160

Arg Ser Lys Leu Asp Cys Leu Glu Asn Leu Glu Tyr Leu Leu His Gln
                165                 170                 175

Ile Asp Asn Ala Leu Met Phe Ile Asp Asn Gly Gly Leu Asp Asp Val
            180                 185                 190

Leu Leu Pro Ile Val Val Asn Asp Thr Ser Thr Ser Leu Arg Val Ser
        195                 200                 205

Ala Met Arg Val Leu Gly Ser Leu Ala Ser Asn Asn Pro Lys Ala Gln
    210                 215                 220

Ile Lys Val Phe Glu Lys Asn Phe Gly Ser His Leu Ala Gln Ile Leu
225                 230                 235                 240

Thr Ser Ser Gly Asn Val Gly Glu Ile Ser Ala Ala Leu His Ala Phe
                245                 250                 255

Gly Ala Leu Leu Arg Lys Phe Pro Leu Ala Gln Gln Arg Val Leu Ser
            260                 265                 270

Thr Ser Gly Thr Gln Ala Leu Ile Lys Val Leu Gln Ser Pro Asp Val
        275                 280                 285

Glu Leu Arg Ser Lys Ala Lys Val Val Thr Leu Ile Ser Asp Leu Val
    290                 295                 300

Leu Glu Lys Arg Ser Val Leu Asp Val Ser Lys Asp Asp Pro Glu Ala
305                 310                 315                 320

Ser Ser Thr Met Ala Gln Tyr Val Leu Leu Asp Phe Glu Ser Trp Leu
                325                 330                 335

Lys Thr Pro Gly Tyr Cys Ala Ala Val Asp Thr Val Leu Thr Lys Glu
            340                 345                 350

Phe Leu Leu Leu Leu Glu Gln Pro Glu Val Val Glu Gln Phe Ala Thr
        355                 360                 365

Ala Leu Glu Thr Thr Glu Asp Met Cys Thr Ser Thr Trp Ser Gln Ser
    370                 375                 380

Ser Gly Leu Arg His Ala Leu Leu Thr Val Arg Asn Arg Tyr Ala Asn
385                 390                 395                 400

Ser Thr Asp Glu Tyr Arg Leu Glu Val Ser Gln Ile Leu Ala Lys Leu
                405                 410                 415

Cys Glu Arg Leu Phe Asn Lys Pro Lys His Thr Glu Leu
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420 425

<210> 55
<211> 336
<212> DNA
<213> Drosophila melanogaster

<400> 55
atggtggccg ttaagaaaca aaagaaggct ctggagagca ccaacgcccg tctggcgctg 60

gtgatgaagt ccggcaaata ctgcctgggc tacaagcaga ccttgaagac cctgcgccag 120

ggcaaggcca aactggtgct catcgccagc aacacgcccg ccctgaggaa gtccgagatc 180

gagtactacg ctatgctggc caagactgaa gtccagcact acagcggcac caacatcgag 240

ctgggcaccg cctgtggtaa atacttccgc gtgtgcaccc tgtccatcac cgatcctgga 300

gattcggaca tcatccgctc gctggagacg gcctaa 336

<210> 56
<211> 111
<212> PRT
<213> Drosophila melanogaster

<400> 56

Met Val Ala Val Lys Lys Gln Lys Lys Ala Leu Glu Ser Thr Asn Ala
1 5 10 15

Arg Leu Ala Leu Val Met Lys Ser Gly Lys Tyr Cys Leu Gly Tyr Lys
20 25 30

Gln Thr Leu Lys Thr Leu Arg Gln Gly Lys Ala Lys Leu Val Leu Ile
35 40 45

Ala Ser Asn Thr Pro Ala Leu Arg Lys Ser Glu Ile Glu Tyr Tyr Ala
50 55 60

Met Leu Ala Lys Thr Glu Val Gln His Tyr Ser Gly Thr Asn Ile Glu
65 70 75 80

Leu Gly Thr Ala Cys Gly Lys Tyr Phe Arg Val Cys Thr Leu Ser Ile
85 90 95

Thr Asp Pro Gly Asp Ser Asp Ile Ile Arg Ser Leu Glu Thr Ala
100 105 110

<210> 57
<211> 822
<212> DNA
<213> Drosophila melanogaster

<400> 57
atggctcact tcgcgatgac accaaacata cgtcacaaca acaaaaacaa caacaacaac 60

aacgacaaga tgtggcagca tgtgcacaaa tgcaatccgg ttcgcttgcc cgccaagcta 120

gacgagcaaa aaatgtttat ttttaacaat attccacaga ttatcatctg tcgtcgtctg 180

atgcacttcg atgaatgggc gacgcttcct ttcgctcgcc atccgccgcg atccgctgac 240

gccgcccatt ccggcagcaa gaactcaaac gttgcgaacg gaagcgaaat gcaagtggaa 300

tcgagctata ccaaatatgc cggacgtgtg ccacctttgg acctcaccca ggtgaatggt 360

ggccaagatt tgtggggcgg caatggtggc ggcaataacg catccgccag acgccatctg 420

catcatccct atcaaatgct ggacaagtgc cgcggcggag taaccctgat cagtgcatca 480

tccgccatct catctacatc caactcctcc gacgacaata acaatcgact gatgagcgct 540

gatgatggca ccaccagtct gctgcatccc ttgggctccg atggtctgcc tctggatccg 600

cgcgattgga cgcgagcgga tgtctggaaa tggctcatca atatggccgt atccgaggga 660

ttggaggtca ccgccgaact gccacagaaa ttccccatga acggcaaggc attgtgcctg 720

atgagtctcg atatgtacct gtgccgagtt cccgtgggcg gcaagatgct ctaccgcgac 780

ttccgggtgc gactcgcccg agcaatggcc ctgctatcat ag 822

<210> 58
<211> 273
<212> PRT
<213> Drosophila melanogaster

<400> 58

Met Ala His Phe Ala Met Thr Pro Asn Ile Arg His Asn Asn Lys Asn
1 5 10 15

Asn Asn Asn Asn Asn Asp Lys Met Trp Gln His Val His Lys Cys Asn
20 25 30

Pro Val Arg Leu Pro Ala Lys Leu Asp Glu Gln Lys Met Phe Ile Phe
35 40 45

Asn Asn Ile Pro Gln Ile Ile Ile Cys Arg Arg Leu Met His Phe Asp
50 55 60

Glu Trp Ala Thr Leu Pro Phe Ala Arg His Pro Pro Arg Ser Ala Asp
65 70 75 80

Ala Ala His Ser Gly Ser Lys Asn Ser Asn Val Ala Asn Gly Ser Glu
85 90 95

Met Gln Val Glu Ser Ser Tyr Thr Lys Tyr Ala Gly Arg Val Pro Pro
100 105 110

Leu Asp Leu Thr Gln Val Asn Gly Gly Gln Asp Leu Trp Gly Gly Asn
115 120 125

Gly Gly Gly Asn Asn Ala Ser Ala Arg Arg His Leu His His Pro Tyr
130 135 140

Gln Met Leu Asp Lys Cys Arg Gly Gly Val Thr Leu Ile Ser Ala Ser
145 150 155 160

Ser Ala Ile Ser Ser Thr Ser Asn Ser Ser Asp Asp Asn Asn Asn Arg

165 170 175

Leu Met Ser Ala Asp Asp Gly Thr Thr Ser Leu Leu His Pro Leu Gly
180 185 190

Ser Asp Gly Leu Pro Leu Asp Pro Arg Asp Trp Thr Arg Ala Asp Val
195 200 205

Trp Lys Trp Leu Ile Asn Met Ala Val Ser Glu Gly Leu Glu Val Thr
210 215 220

Ala Glu Leu Pro Gln Lys Phe Pro Met Asn Gly Lys Ala Leu Cys Leu
225 230 235 240

Met Ser Leu Asp Met Tyr Leu Cys Arg Val Pro Val Gly Gly Lys Met
245 250 255

Leu Tyr Arg Asp Phe Arg Val Arg Leu Ala Arg Ala Met Ala Leu Leu
260 265 270

Ser

<210> 59
<211> 1341
<212> DNA
<213> Drosophila melanogaster

<400> 59
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gacaccattg agaatgttaa ggctaagatc caagacaagg aaggaattcc cccagatcag 120

cagcgtctga tcttcgccgg caagcaactg gaagacggac gcaccctgtc cgattacaac 180

attcagaagg agtccaccct tcacttggtc cttcgtctcc gtggtggtat gcagatcttc 240

gtgaagactt tgaccggaaa gaccatcacc ctcgaggtag agccatcgga caccattgag 300

aataaggagt ccacccttca cttggtcctt cgtctccgtg gtggtatgca gatcttcgtg 360

aagactttga ccggaaagac catcaccctc gaggtagagc catcggacac aattgagaat 420

gttaaggcta agatccaaga caaggaggga attcccccag atcagcagcg tctgatcttc 480

gccggcaagc agcttgagga tggacgcacc ctgtccgatt acaacatcca gaaggagtcc 540

acccttcact tggtccttcg tctccgtggt ggtatgcaga tcttcgtgaa gactttgacc 600

ggaaagacca tcaccctcga ggtagagcct tcggacacca ttgagaatgt taaggctaag 660

atccaagaca aggagggaat tcccccagat cagcagcgtc tgatcttcgc cggcaagcag 720

cttgaggatg gacgcaccct gtccgattac aacattcaga aggagtccac ccttcacttg 780

gtccttcgtc ttcgtggtgg tatgcagatc ttcgtgaaga ctttgaccgg aaagaccatc 840

accctcgagg tagagccatc ggacacaatt gagaatgtta aggctaagat ccaagacaag 900

gagggaattc ccccagatca gcagcgtctg atcttcgccg gcaagcagct tgaggatgga 960

cgcaccctgt ccgattacaa catccagaag gagtccaccc ttcacttggt ccttcgtctc 1020

cgtggtggta tgcagatctt cgccaagatt caagataagg agggaatccc cccagatcag 1080

cagcgtctga tcttcgccgg caagcagctt gaggatggac gcaccctgtc cgattacaac 1140

atccagaagg agtccaccct tcacttggtc cttcgtctcc gtggtggtat gcagatcttc 1200

gtgaagactt tgaccggaaa gaccatcacc ctcgaggtag agccttcgga caccattgag 1260

aatgttaagg ctaagatcca agacaaggag ggaattcccc cagatcagca gcagtctgat 1320

cttcgccggc aagcagcttg a 1341

<210> 60
<211> 446
<212> PRT
<213> Drosophila melanogaster

<400> 60

Met Gln Ile Phe Val Lys Thr Leu Thr Gly Lys Thr Ile Thr Leu Glu
1 5 10 15

Val Glu Pro Ser Asp Thr Ile Glu Asn Val Lys Ala Lys Ile Gln Asp
20 25 30

Lys Glu Gly Ile Pro Pro Asp Gln Gln Arg Leu Ile Phe Ala Gly Lys
35 40 45

Gln Leu Glu Asp Gly Arg Thr Leu Ser Asp Tyr Asn Ile Gln Lys Glu
50 55 60

Ser Thr Leu His Leu Val Leu Arg Leu Arg Gly Gly Met Gln Ile Phe
65 70 75 80

Val Lys Thr Leu Thr Gly Lys Thr Ile Thr Leu Glu Val Glu Pro Ser
85 90 95

Asp Thr Ile Glu Asn Lys Glu Ser Thr Leu His Leu Val Leu Arg Leu
100 105 110

Arg Gly Gly Met Gln Ile Phe Val Lys Thr Leu Thr Gly Lys Thr Ile
115 120 125

Thr Leu Glu Val Glu Pro Ser Asp Thr Ile Glu Asn Val Lys Ala Lys
130 135 140

Ile Gln Asp Lys Glu Gly Ile Pro Pro Asp Gln Gln Arg Leu Ile Phe
145 150 155 160

Ala Gly Lys Gln Leu Glu Asp Gly Arg Thr Leu Ser Asp Tyr Asn Ile
165 170 175

Gln Lys Glu Ser Thr Leu His Leu Val Leu Arg Leu Arg Gly Gly Met
180 185 190

Gln Ile Phe Val Lys Thr Leu Thr Gly Lys Thr Ile Thr Leu Glu Val
195 200 205

```
Glu Pro Ser Asp Thr Ile Glu Asn Val Lys Ala Lys Ile Gln Asp Lys
    210                 215                 220

Glu Gly Ile Pro Pro Asp Gln Gln Arg Leu Ile Phe Ala Gly Lys Gln
225                 230                 235                 240

Leu Glu Asp Gly Arg Thr Leu Ser Asp Tyr Asn Ile Gln Lys Glu Ser
                245                 250                 255

Thr Leu His Leu Val Leu Arg Leu Arg Gly Gly Met Gln Ile Phe Val
            260                 265                 270

Lys Thr Leu Thr Gly Lys Thr Ile Thr Leu Glu Val Glu Pro Ser Asp
        275                 280                 285

Thr Ile Glu Asn Val Lys Ala Lys Ile Gln Asp Lys Glu Gly Ile Pro
    290                 295                 300

Pro Asp Gln Gln Arg Leu Ile Phe Ala Gly Lys Gln Leu Glu Asp Gly
305                 310                 315                 320

Arg Thr Leu Ser Asp Tyr Asn Ile Gln Lys Glu Ser Thr Leu His Leu
                325                 330                 335

Val Leu Arg Leu Arg Gly Gly Met Gln Ile Phe Ala Lys Ile Gln Asp
            340                 345                 350

Lys Glu Gly Ile Pro Pro Asp Gln Gln Arg Leu Ile Phe Ala Gly Lys
        355                 360                 365

Gln Leu Glu Asp Gly Arg Thr Leu Ser Asp Tyr Asn Ile Gln Lys Glu
    370                 375                 380

Ser Thr Leu His Leu Val Leu Arg Leu Arg Gly Gly Met Gln Ile Phe
385                 390                 395                 400

Val Lys Thr Leu Thr Gly Lys Thr Ile Thr Leu Glu Val Glu Pro Ser
                405                 410                 415

Asp Thr Ile Glu Asn Val Lys Ala Lys Ile Gln Asp Lys Glu Gly Ile
            420                 425                 430

Pro Pro Asp Gln Gln Gln Ser Asp Leu Arg Arg Gln Ala Ala
        435                 440                 445
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<210> 61
<211> 1884
<212> DNA
<213> Drosophila melanogaster

<400> 61

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atgaaataca tcctggtaac tggtggcgtc attagtggcg tgggaaaagg agtgattgcc     60

tcctcgttcg gaacgctttt gaaatcctgt ggtctggatg taacctcgat caagattgac    120

ccctatatca atatagatgc tggaaccttt tcgccttatg agcatggcga ggtttacgtt    180

ttggacgatg gcgccgaggt ggatctggat ctgggaaact atgaacggtt tttggatgtt    240

accctgcatc gggacaacaa cataaccacc ggaaaaattt acaagttggt cattgagaag    300
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gagcgcactg gcgagtactt gggcaaaacg gttcaagttg tcccacacat cactgatgcc 360

attcaggaat gggtggagcg cgtggcccag acacccgttc agggatcttc aaagccacag 420

gtgtgcatcg tggaattggg aggaacgatt ggtgacatcg aaggcatgcc tttcgtagag 480

gccttccgtc agtttcagtt ccgcgtaaag agagagaact tctgtttggc ccatgtgtcg 540

ctggttccgt tgccaaaggc taccggagaa cccaagacca agcccacaca aagttcggtc 600

agagaactga gaggatgtgg cctgagtccc gatttgattg tctgccgatc ggagaaaccc 660

attggactgg aggtcaagga gaagatcagc aacttttgtc atgtggggcc ggatcaggtg 720

atatgcatcc acgatttgaa ctccatttat catgttccgc tgctgatgga gcagaatggt 780

gttattgaat acctaaatga gcgcctacag cttaatatcg acatgagcaa gaggaccaaa 840

tgcttgcagc aatggcgaga tttggcgcgt cgaacggaga ccgttcgccg tgaagtttgc 900

atcgccgtcg tgggaaagta caccaagttc acggattcgt acgcctccgt agttaaagcc 960

ctgcaacatg ccgccctggc agtgaatcgc aaactggaac tggtctttat cgagtcgtgc 1020

ctgctggagg aggaaacttt gcattctgag ccgagcaagt accacaagga gtggcagaag 1080

ctatgcgata gccatggcat cctagtcccc ggtggattcg gttcccgtgg aatggagggc 1140

aagattcgtg catgccaatg ggcgcgagag aatcaaaagc cattgcttgg catctgcttg 1200

ggtctgcaag cggcggtcat tgaattcgca cgaaataaac ttggtctcaa ggatgcaaac 1260

accacagaaa tcgatccgaa cacagctaat gccttggtca tcgatatgcc agagcatcac 1320

acgggtcaat tgggcggcac tatgcgcttg ggcaagcgaa taactgtttt ctctgatggt 1380

cctagtgtca ttcgccagtt gtatggcaat ccgaaaagcg tgcaggagcg tcatcggcat 1440

cgttacgagg ttaatcccaa atacgtgcat ctgctggaag agcaaggcat gcgatttgtg 1500

ggcaccgacg tcgacaaaac taggatggaa atcattgagc tcagcggtca tccctacttt 1560

gttgccaccc aatatcatcc agagtacttg tcgcggcctc tgaagccgtc gcctcctttc 1620

ctcggcctga tcctggcctc agtggatcga ttgaaccaat atattcagcg cggttgccgc 1680

ctgtcgcccc gccagctatc cgacgcatcc tcggatgagg aggacagtgt tgtgggcttg 1740

gccggagcaa caaaatcgct gagctccttg aaaattccca ttacacccac aaatggaata 1800

tcaaaaagtt gcaatggtag cataagcact tccgacagcg aaggtgcctg cggaggcgtt 1860

gatcctacca atggccataa gtaa 1884

<210> 62
<211> 627
<212> PRT
<213> Drosophila melanogaster

<400> 62

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Met Lys Tyr Ile Leu Val Thr Gly Gly Val Ile Ser Gly Val Gly Lys
1               5                  10                  15

Gly Val Ile Ala Ser Ser Phe Gly Thr Leu Leu Lys Ser Cys Gly Leu
            20                  25                  30

Asp Val Thr Ser Ile Lys Ile Asp Pro Tyr Ile Asn Ile Asp Ala Gly
        35                  40                  45

Thr Phe Ser Pro Tyr Glu His Gly Glu Val Tyr Val Leu Asp Asp Gly
    50                  55                  60

Ala Glu Val Asp Leu Asp Leu Gly Asn Tyr Glu Arg Phe Leu Asp Val
65                  70                  75                  80

Thr Leu His Arg Asp Asn Asn Ile Thr Thr Gly Lys Ile Tyr Lys Leu
                85                  90                  95

Val Ile Glu Lys Glu Arg Thr Gly Glu Tyr Leu Gly Lys Thr Val Gln
            100                 105                 110

Val Val Pro His Ile Thr Asp Ala Ile Gln Glu Trp Val Glu Arg Val
        115                 120                 125

Ala Gln Thr Pro Val Gln Gly Ser Ser Lys Pro Gln Val Cys Ile Val
    130                 135                 140

Glu Leu Gly Gly Thr Ile Gly Asp Ile Glu Gly Met Pro Phe Val Glu
145                 150                 155                 160

Ala Phe Arg Gln Phe Gln Phe Arg Val Lys Arg Glu Asn Phe Cys Leu
                165                 170                 175

Ala His Val Ser Leu Val Pro Leu Pro Lys Ala Thr Gly Glu Pro Lys
            180                 185                 190

Thr Lys Pro Thr Gln Ser Ser Val Arg Glu Leu Arg Gly Cys Gly Leu
        195                 200                 205

Ser Pro Asp Leu Ile Val Cys Arg Ser Glu Lys Pro Ile Gly Leu Glu
    210                 215                 220

Val Lys Glu Lys Ile Ser Asn Phe Cys His Val Gly Pro Asp Gln Val
225                 230                 235                 240

Ile Cys Ile His Asp Leu Asn Ser Ile Tyr His Val Pro Leu Leu Met
                245                 250                 255

Glu Gln Asn Gly Val Ile Glu Tyr Leu Asn Glu Arg Leu Gln Leu Asn
            260                 265                 270

Ile Asp Met Ser Lys Arg Thr Lys Cys Leu Gln Gln Trp Arg Asp Leu
        275                 280                 285

Ala Arg Arg Thr Glu Thr Val Arg Arg Glu Val Cys Ile Ala Val Val
    290                 295                 300

Gly Lys Tyr Thr Lys Phe Thr Asp Ser Tyr Ala Ser Val Val Lys Ala
305                 310                 315                 320
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Leu Gln His Ala Ala Leu Ala Val Asn Arg Lys Leu Glu Leu Val Phe
                325                 330                 335

Ile Glu Ser Cys Leu Leu Glu Glu Glu Thr Leu His Ser Glu Pro Ser
            340                 345                 350

Lys Tyr His Lys Glu Trp Gln Lys Leu Cys Asp Ser His Gly Ile Leu
        355                 360                 365

Val Pro Gly Gly Phe Gly Ser Arg Gly Met Glu Gly Lys Ile Arg Ala
    370                 375                 380

Cys Gln Trp Ala Arg Glu Asn Gln Lys Pro Leu Leu Gly Ile Cys Leu
385                 390                 395                 400

Gly Leu Gln Ala Ala Val Ile Glu Phe Ala Arg Asn Lys Leu Gly Leu
                405                 410                 415

Lys Asp Ala Asn Thr Thr Glu Ile Asp Pro Asn Thr Ala Asn Ala Leu
            420                 425                 430

Val Ile Asp Met Pro Glu His His Thr Gly Gln Leu Gly Gly Thr Met
        435                 440                 445

Arg Leu Gly Lys Arg Ile Thr Val Phe Ser Asp Gly Pro Ser Val Ile
    450                 455                 460

Arg Gln Leu Tyr Gly Asn Pro Lys Ser Val Gln Glu Arg His Arg His
465                 470                 475                 480

Arg Tyr Glu Val Asn Pro Lys Tyr Val His Leu Leu Glu Glu Gln Gly
                485                 490                 495

Met Arg Phe Val Gly Thr Asp Val Asp Lys Thr Arg Met Glu Ile Ile
            500                 505                 510

Glu Leu Ser Gly His Pro Tyr Phe Val Ala Thr Gln Tyr His Pro Glu
        515                 520                 525

Tyr Leu Ser Arg Pro Leu Lys Pro Ser Pro Pro Phe Leu Gly Leu Ile
    530                 535                 540

Leu Ala Ser Val Asp Arg Leu Asn Gln Tyr Ile Gln Arg Gly Cys Arg
545                 550                 555                 560

Leu Ser Pro Arg Gln Leu Ser Asp Ala Ser Ser Asp Glu Glu Asp Ser
                565                 570                 575

Val Val Gly Leu Ala Gly Ala Thr Lys Ser Leu Ser Ser Leu Lys Ile
            580                 585                 590

Pro Ile Thr Pro Thr Asn Gly Ile Ser Lys Ser Cys Asn Gly Ser Ile
        595                 600                 605

Ser Thr Ser Asp Ser Glu Gly Ala Cys Gly Gly Val Asp Pro Thr Asn
    610                 615                 620

Gly His Lys
625
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<210> 63

<211> 1905
<212> DNA
<213> Drosophila melanogaster

<400> 63
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ataacgagcg ccgacggcac gcaatcaacg gcaaagagca agtacaaaga cggcagtgcc 120

catccgcatc aaggcagcga cgcgcagtat taccacacgg tgacggcggt gcgtccaaac 180

tcttcccaac ggtcgccgat gaccaaggtc atggatctgt tccggcatcg atccagctcg 240

gttgtcagcg aagccgacaa acgcaaagcg gctcacatgc gtcgtgcctc cgcggatttg 300

gagaaacgtc gtgcatcagt tggtgccgca ggtcgaggac tgcgagggga tggtactttg 360

gatccacacc atgcagccat cctcttcaga gactcacgag ggttgcctgt cgctgatccg 420

ttcctagaga aagtaaatct atcagatctg gaagaggacg actcacagat cttcgtgaag 480

ttctttcgtt ttcacaagtg ctatgatctg atacccacct ccgccaagtt ggttgtcttc 540

gacacccagc ttcttgtaaa gaaggccttc tacgccctcg tctacaacgg tgtgcgagcg 600

gcaccgctct gggattcgga gaagcaacag ttcgtgggca tgctaaccat cacggacttt 660

atcaagatcc tgcaaatgta ttacaaatcg ccaaatgcgt ccatggagca gctggaagag 720

cacaaactgg acacgtggcg gagcgtgctg cacaaccagg tgatgccgtt ggtcagcatc 780

ggaccggatg cgtccctcta cgatgccatc aaaattctca tccacagccg catacatcgc 840

ctgcccgtca tcgatccggc gaccggcaat gtcctctaca tcctgacaca taaacgcata 900

cttaggttcc ttttcctata cattaatgaa ttaccaaagc ccgcgtacat gcaaaaaagt 960

ttgcgcgaac tgaagattgg cacctataac aacatcgaga ccgccgacga gacgacgagc 1020

atcatcacgg cgctcaagaa atttgtggag cgacgagtct cagccctgcc actagtggat 1080

tccgatggtc gcctcgttga catttacgca aagtttgatg tgattaatct cgccgccgag 1140

aaaacctaca acgatctcga tgtttcgctg cgcaaagcca acgagcaccg gaacgagtgg 1200

ttcgagggcg tgcagaagtg caatctggac gaatcgctct acacgatcat ggaacgaatc 1260

gtccgcgccg aagtacatcg actggtggtg gtcgacgaga atcgcaaagt gatcggcatt 1320

atctcgctgt ccgatatact gctctacctc gtcctgcgac caagcggtga aggcgtcggt 1380

ggctcggaga gctcattgcg tgcgtccgat cccgttctgc tgcgcaaagt ggctgaggtt 1440

gaaataccag cgacagccgc agcggcgacg acaacaaccc cgcctcgcag tccatcggcc 1500

ggatccggca atcgcagcct gatcgaggac atacccgaag aggagacggc gccggcgagg 1560

agcgacgatg ccgacagtga taacaataag tccgccagtg aggataaagc caacaataac 1620

cagcacgacc agacgacgac ggctgcgaca gctaatggtg atagcaacaa cagccccgta 1680

gaagtgtcct ttgccgatga ggcgcaggaa gaagaagctg ccgaccaggt cgagcgcagc 1740

aattgtgatg atgatgacca gccagcgtta gcggagattg agcgcaagaa tgcatcgatg 1800

gacgacgacg aggacgatgg gatgagcagc gccgtgtccg ctgcctccgc tttgggccag 1860

tcactgacgc ccgcggcgca agaaatggcg ttggttagtg aataa 1905

<210> 64
<211> 634
<212> PRT
<213> Drosophila melanogaster

<400> 64

Met Asn Ser Met Lys Val Ala Met Gln Asn Phe Ser His Arg Gln His
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Pro Ala Val Thr Ile Thr Ser Ala Asp Gly Thr Gln Ser Thr Ala Lys
20 25 30

Ser Lys Tyr Lys Asp Gly Ser Ala His Pro His Gln Gly Ser Asp Ala
35 40 45

Gln Tyr Tyr His Thr Val Thr Ala Val Arg Pro Asn Ser Ser Gln Arg
50 55 60

Ser Pro Met Thr Lys Val Met Asp Leu Phe Arg His Arg Ser Ser Ser
65 70 75 80

Val Val Ser Glu Ala Asp Lys Arg Lys Ala Ala His Met Arg Arg Ala
85 90 95

Ser Ala Asp Leu Glu Lys Arg Arg Ala Ser Val Gly Ala Ala Gly Arg
100 105 110

Gly Leu Arg Gly Asp Gly Thr Leu Asp Pro His His Ala Ala Ile Leu
115 120 125

Phe Arg Asp Ser Arg Gly Leu Pro Val Ala Asp Pro Phe Leu Glu Lys
130 135 140

Val Asn Leu Ser Asp Leu Glu Glu Asp Asp Ser Gln Ile Phe Val Lys
145 150 155 160

Phe Phe Arg Phe His Lys Cys Tyr Asp Leu Ile Pro Thr Ser Ala Lys
165 170 175

Leu Val Val Phe Asp Thr Gln Leu Leu Val Lys Lys Ala Phe Tyr Ala
180 185 190

Leu Val Tyr Asn Gly Val Arg Ala Ala Pro Leu Trp Asp Ser Glu Lys
195 200 205

Gln Gln Phe Val Gly Met Leu Thr Ile Thr Asp Phe Ile Lys Ile Leu
210 215 220

Gln Met Tyr Tyr Lys Ser Pro Asn Ala Ser Met Glu Gln Leu Glu Glu
225 230 235 240

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His Lys Leu Asp Thr Trp Arg Ser Val Leu His Asn Gln Val Met Pro
                245                 250                 255

Leu Val Ser Ile Gly Pro Asp Ala Ser Leu Tyr Asp Ala Ile Lys Ile
            260                 265                 270

Leu Ile His Ser Arg Ile His Arg Leu Pro Val Ile Asp Pro Ala Thr
        275                 280                 285

Gly Asn Val Leu Tyr Ile Leu Thr His Lys Arg Ile Leu Arg Phe Leu
    290                 295                 300

Phe Leu Tyr Ile Asn Glu Leu Pro Lys Pro Ala Tyr Met Gln Lys Ser
305                 310                 315                 320

Leu Arg Glu Leu Lys Ile Gly Thr Tyr Asn Asn Ile Glu Thr Ala Asp
                325                 330                 335

Glu Thr Thr Ser Ile Ile Thr Ala Leu Lys Lys Phe Val Glu Arg Arg
            340                 345                 350

Val Ser Ala Leu Pro Leu Val Asp Ser Asp Gly Arg Leu Val Asp Ile
        355                 360                 365

Tyr Ala Lys Phe Asp Val Ile Asn Leu Ala Ala Glu Lys Thr Tyr Asn
    370                 375                 380

Asp Leu Asp Val Ser Leu Arg Lys Ala Asn Glu His Arg Asn Glu Trp
385                 390                 395                 400

Phe Glu Gly Val Gln Lys Cys Asn Leu Asp Glu Ser Leu Tyr Thr Ile
                405                 410                 415

Met Glu Arg Ile Val Arg Ala Glu Val His Arg Leu Val Val Val Asp
            420                 425                 430

Glu Asn Arg Lys Val Ile Gly Ile Ile Ser Leu Ser Asp Ile Leu Leu
        435                 440                 445

Tyr Leu Val Leu Arg Pro Ser Gly Glu Gly Val Gly Gly Ser Glu Ser
    450                 455                 460

Ser Leu Arg Ala Ser Asp Pro Val Leu Leu Arg Lys Val Ala Glu Val
465                 470                 475                 480

Glu Ile Pro Ala Thr Ala Ala Ala Ala Thr Thr Thr Thr Pro Pro Arg
                485                 490                 495

Ser Pro Ser Ala Gly Ser Gly Asn Arg Ser Leu Ile Glu Asp Ile Pro
            500                 505                 510

Glu Glu Glu Thr Ala Pro Ala Arg Ser Asp Asp Ala Asp Ser Asp Asn
        515                 520                 525

Asn Lys Ser Ala Ser Glu Asp Lys Ala Asn Asn Asn Gln His Asp Gln
    530                 535                 540

Thr Thr Thr Ala Ala Thr Ala Asn Gly Asp Ser Asn Asn Ser Pro Val
545                 550                 555                 560

Glu Val Ser Phe Ala Asp Glu Ala Gln Glu Glu Glu Ala Ala Asp Gln
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565 570 575

Val Glu Arg Ser Asn Cys Asp Asp Asp Asp Gln Pro Ala Leu Ala Glu
580 585 590

Ile Glu Arg Lys Asn Ala Ser Met Asp Asp Asp Glu Asp Asp Gly Met
595 600 605

Ser Ser Ala Val Ser Ala Ala Ser Ala Leu Gly Gln Ser Leu Thr Pro
610 615 620

Ala Ala Gln Glu Met Ala Leu Val Ser Glu
625 630

<210> 65
<211> 2430
<212> DNA
<213> Drosophila melanogaster

<400> 65
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atcgtggtat ccaatcggtt gccgtttgtg cttatccgag atccgaagac cgatgagttg 120

gaacgcaggg ccagtgccgg tggcctggtg actgcagtgt gcccggtggt gatcaagggc 180

agtggtctct gggtgggctg gtcgggtatc cacttgaagg atcctaacga ggccattccc 240

gagtccaatc ccaacgatca gactccgact gctggcctca agtccgagca ggtggtgtcc 300

gtcaacatcg attcgaagat cttcgatagc tactacaacg gatgctgcaa caagatcttc 360

tggccactgt tccactcgat gccgggaaga gccaacttcg gaggcgagca ctggcacgac 420

tatgtcactg tcaacaagca cttcgccgtg cggaccatcg aggctctgga gaagtgcctg 480

gccaaaaacc agggcagcga gaagagtcca ccgattgtct ggatccacga ctaccatctc 540

atgctggccg ccaattgggt gcgcgagcac gccgaggaga agaacctgcc ctgccgactg 600

gctttcttcc tgcacatccc attcccgcca tgggacatct tccgcctgct gccctggtcc 660

gatgagatcc tacagggtat gttgggttgt gacctggtag gcttccatat tcaggactat 720

tgccttaact ttgtggactg ctgccagcgc aatctcggct gccgtgtgga cagaaacaat 780

ctgctggtgg aacatggcgg gcgcaccgtt cgcgtccgcc cgcttcccat tggtattccc 840

tacgaacgct tcgttaattt ggccacgacc gcgcccaagg tgctaaagac atccaagatg 900

caaatcatcc tgggagtgga ccgactggac tacaccaagg gcctcgtcca tcgccttatg 960

gcttttgagg cgctgctgct gaagtatccg cagcacaagg agaaggtgag cctgctgcag 1020

atctcggtgc cgtcgcgaac cgatgtaaaa gagtaccggg agctgaagga ggaggtggac 1080

cagctggtgg gccgcatcaa cggacgcttt accacagcca actgggcgcc catacgctac 1140

atctacgact atgtcagcca agacgagttg gctgctttgt acagggatgc ggctgtttgc 1200

ctggtaactc cacttcgcga tggcatgaac ctggtggcca aggagttcgt ggcctgccag 1260

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gcactgacca tgcccgagga tgagcgcgtc ctacgtatgg ctcggctgcg ccgtcgtgaa 1440

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ttactgaaat acatcggcta taaccacaag ttggctctgc tgctggacta cgacggaacc 1620

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gagatccttc atccggacgg cagcaagttc gtacacccca tgcccatgga gtacgaaaag 1860

aaggtcagtg acctgctgaa ggctctgcag gattccgttt gccgcgacgg cgcttgggtg 1920

gagaataagg gggcgttgct aacgttccac taccgagaga cgcccaatca tctgagggga 1980

gctatggttg acaaggcgcg ctccttgatc gagaagtacg gcttcaaggc cacggaggcg 2040

cattgcgctc tggaagctcg tccgccggtg cagtggaata agggtcgtgc ctcgatctac 2100

atcctgcgca catccttcgg cgtggactgg aacgaacgca tcaagattat ctatgtgggt 2160

gacgatctaa cagacgagga cgccatggtg gctctgaagg gtatggcgcg aactttccgt 2220

gtgacatcgt cggatattgt gaagaccgct gcggatcatc gactgccctc cacagactcc 2280

gtgtacaccc tgctgaaatg ggtggaacga cacttcatgg gacgcaaggc gcgcgccaat 2340

tcgctgacct acaggcccac caagggcgac ggtgtccaga tgcagatgtc cctggaggtg 2400

gccgcttcag cgaacaatct ggaggtgtga 2430

<210> 66
<211> 809
<212> PRT
<213> Drosophila melanogaster

<400> 66

Met Pro Asp Thr Glu Ile Ile Val Thr Asn Ala Gly Glu Pro Ser Thr
1 5 10 15

Lys Ala Ser Leu Ile Val Val Ser Asn Arg Leu Pro Phe Val Leu Ile
20 25 30

Arg Asp Pro Lys Thr Asp Glu Leu Glu Arg Arg Ala Ser Ala Gly Gly
35 40 45

Leu Val Thr Ala Val Cys Pro Val Val Ile Lys Gly Ser Gly Leu Trp
50 55 60

Val Gly Trp Ser Gly Ile His Leu Lys Asp Pro Asn Glu Ala Ile Pro
65 70 75 80

Glu Ser Asn Pro Asn Asp Gln Thr Pro Thr Ala Gly Leu Lys Ser Glu
85 90 95

Gln Val Val Ser Val Asn Ile Asp Ser Lys Ile Phe Asp Ser Tyr Tyr
100 105 110

Asn Gly Cys Cys Asn Lys Ile Phe Trp Pro Leu Phe His Ser Met Pro
115 120 125

Gly Arg Ala Asn Phe Gly Gly Glu His Trp His Asp Tyr Val Thr Val
130 135 140

Asn Lys His Phe Ala Val Arg Thr Ile Glu Ala Leu Glu Lys Cys Leu
145 150 155 160

Ala Lys Asn Gln Gly Ser Glu Lys Ser Pro Pro Ile Val Trp Ile His
165 170 175

Asp Tyr His Leu Met Leu Ala Ala Asn Trp Val Arg Glu His Ala Glu
180 185 190

Glu Lys Asn Leu Pro Cys Arg Leu Ala Phe Phe Leu His Ile Pro Phe
195 200 205

Pro Pro Trp Asp Ile Phe Arg Leu Leu Pro Trp Ser Asp Glu Ile Leu
210 215 220

Gln Gly Met Leu Gly Cys Asp Leu Val Gly Phe His Ile Gln Asp Tyr
225 230 235 240

Cys Leu Asn Phe Val Asp Cys Cys Gln Arg Asn Leu Gly Cys Arg Val
245 250 255

Asp Arg Asn Asn Leu Leu Val Glu His Gly Gly Arg Thr Val Arg Val
260 265 270

Arg Pro Leu Pro Ile Gly Ile Pro Tyr Glu Arg Phe Val Asn Leu Ala
275 280 285

Thr Thr Ala Pro Lys Val Leu Lys Thr Ser Lys Met Gln Ile Ile Leu
290 295 300

Gly Val Asp Arg Leu Asp Tyr Thr Lys Gly Leu Val His Arg Leu Met
305 310 315 320

Ala Phe Glu Ala Leu Leu Leu Lys Tyr Pro Gln His Lys Glu Lys Val
325 330 335

Ser Leu Leu Gln Ile Ser Val Pro Ser Arg Thr Asp Val Lys Glu Tyr
340 345 350

Arg Glu Leu Lys Glu Glu Val Asp Gln Leu Val Gly Arg Ile Asn Gly
355 360 365

Arg Phe Thr Thr Ala Asn Trp Ala Pro Ile Arg Tyr Ile Tyr Asp Tyr
370 375 380

Val Ser Gln Asp Glu Leu Ala Ala Leu Tyr Arg Asp Ala Ala Val Cys

385 390 395 400

Leu Val Thr Pro Leu Arg Asp Gly Met Asn Leu Val Ala Lys Glu Phe
405 410 415

Val Ala Cys Gln Ile Asn Glu Val Pro Gly Val Leu Val Ile Ser Pro
420 425 430

Phe Ala Gly Ala Gly Glu Met Met His Glu Ala Leu Leu Cys Asn Pro
435 440 445

Tyr Glu Val Asn Glu Ala Ala Glu Val Ile His Arg Ala Leu Thr Met
450 455 460

Pro Glu Asp Glu Arg Val Leu Arg Met Ala Arg Leu Arg Arg Arg Glu
465 470 475 480

Ala Glu Cys Asp Val Ser His Trp Met Arg Cys Phe Leu Lys Ala Val
485 490 495

Gly Ala Leu Glu Met Asp Asp Val Gly Thr Thr Ile Met Gln Pro Val
500 505 510

Ser Val Asp Asp Phe Asp Asp Tyr Leu Leu Lys Tyr Ile Gly Tyr Asn
515 520 525

His Lys Leu Ala Leu Leu Leu Asp Tyr Asp Gly Thr Leu Ala Pro Ile
530 535 540

Ala Pro His Pro Asp Leu Ala Thr Leu Ser Pro Glu Ile Lys Asn Val
545 550 555 560

Leu Tyr Lys Leu Ser Asn His Ser Asp Val Tyr Val Ala Val Ile Ser
565 570 575

Gly Arg Asn Val Asp Asn Val Lys Lys Met Val Gly Ile Glu Gly Ile
580 585 590

Thr Tyr Ala Gly Asn His Gly Leu Glu Ile Leu His Pro Asp Gly Ser
595 600 605

Lys Phe Val His Pro Met Pro Met Glu Tyr Glu Lys Lys Val Ser Asp
610 615 620

Leu Leu Lys Ala Leu Gln Asp Ser Val Cys Arg Asp Gly Ala Trp Val
625 630 635 640

Glu Asn Lys Gly Ala Leu Leu Thr Phe His Tyr Arg Glu Thr Pro Asn
645 650 655

His Leu Arg Gly Ala Met Val Asp Lys Ala Arg Ser Leu Ile Glu Lys
660 665 670

Tyr Gly Phe Lys Ala Thr Glu Ala His Cys Ala Leu Glu Ala Arg Pro
675 680 685

Pro Val Gln Trp Asn Lys Gly Arg Ala Ser Ile Tyr Ile Leu Arg Thr
690 695 700

Ser Phe Gly Val Asp Trp Asn Glu Arg Ile Lys Ile Ile Tyr Val Gly
705 710 715 720

Asp Asp Leu Thr Asp Glu Asp Ala Met Val Ala Leu Lys Gly Met Ala
725 730 735

Arg Thr Phe Arg Val Thr Ser Ser Asp Ile Val Lys Thr Ala Ala Asp
740 745 750

His Arg Leu Pro Ser Thr Asp Ser Val Tyr Thr Leu Leu Lys Trp Val
755 760 765

Glu Arg His Phe Met Gly Arg Lys Ala Arg Ala Asn Ser Leu Thr Tyr
770 775 780

Arg Pro Thr Lys Gly Asp Gly Val Gln Met Gln Met Ser Leu Glu Val
785 790 795 800

Ala Ala Ser Ala Asn Asn Leu Glu Val
805

<210> 67
<211> 567
<212> DNA
<213> Drosophila melanogaster

<220>
<221> misc_feature
<222> (1)..(567)
<223> n = a, t, c, or g

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gtcttttcgc cgccttttgt tttcgcaatt ttttttgct caatttttaa tgcaatttcc 120

acgcttaact gcacttttg ccatttcgct tgttattcct gtttcttctg atgttgctgt 180

ttctgttttt gcacagcatt tatttacacg aaatacaccc acaatcacac acacaggcac 240

aagctcaagc aaacgcacac aatggcaggc gaccggaaac agacagagac aaaatatgta 300

cacaatttgc agcgctctcg ttccctccgg tgcattccaa attcaaatta ctgttgcagc 360

tcttccagtt atggttatcg ttcgccttgt tccaatcctg caaatcagat ctgagcgctc 420

cggtcgctca tcaagtggcc tttgtcctgc ccgaggactc ggatttgcgg atctgcagat 480

ctggactggg gatctangtc tggactctgt caggagtcga gtcttcgcat cttcttcaag 540

tatctttttc aatatccatg cgatttc 567

<210> 68

<400> 68

000

<210> 69
<211> 528
<212> DNA

<213> Drosophila melanogaster

<220>
<221> misc_feature
<222> (1)..(528)
<223> n = a, t, c, or g

<400> 69
caattgatat ggtacatttg ttgccgtttt ttctttttg gaagtcaccg ccaccgcaaa 60

cgtatacaca tgtaccggat tgtgtacggg ttcatttatt tttaaagcat tcaatgtagt 120

attatgggaa tgtgaaaatt aatcgaagct tatcacctgt tgtactgatc aattttatct 180

atctttccgt ttcgcgtgtg tgggagtgta ttagagatgg ttttagggtt gtcaaactat 240

tgaaaattaa tcgattgtta ccattccagt tacattttaa tgaaatctct ggacattctt 300

cgaaaattgt ttgtttttga ctggcccaat ttaaatgtgt ttatctaagc tcaattacag 360

atgggcatat ttgtatgtag caaataggca atgtgttaat gattgtgatc acagatcacc 420

ttgcatacct gtagtccctc tgcaattaaa tgctttttta gcatatgagg tgaaagtgaa 480

ggtcattaat atttgcatat ggaaatgttt acgcagcgan aatgccga 528

<210> 70

<400> 70

000

<210> 71
<211> 318
<212> DNA
<213> Drosophila melanogaster

<220>
<221> misc_feature
<222> (1)..(318)
<223> n = a, t, c, or g

<400> 71
aaacatccgt cgaaagctaa atgtttcact gatctgaaat gttttcgagt cgataagcat 60

tgtagcattg agcaattaga actttgctcc gataaaggtt tttaaaatac gaagaatata 120

ggagcatagg aacacaaaaa taggaagtac aaaatactat atatactcat ttgagattac 180

agagaacaaa ganaagaagc aatagttana cccacgtaat gataaatatt atctgaaatg 240

agtaactcca gcgtaaatta caaaaattaa tgctgaaaca ctgaatcaca gatgtaaggt 300

agtttccatt cgacccaa 318

<210> 72

<400> 72

000

<210> 73
<211> 687
<212> DNA
<213> Drosophila melanogaster

<400> 73
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tcgctaaact gaagcacaat cgcgttcttt gagtggaaac gccagcacaa ataagaaaca 120

gccccaatca aagtcaaatc aaaacaacac taattcatct ctgcgactgg aaatcaatat 180

tccaattctt caagccaaat aaatagaaaa caaaatccca gtgaagcaag aagtgcattc 240

gattttcctg ctcgtggagc tattggtatt tttaaatcgc tgaccgcaga atatttctac 300

tgcttaaaat agacggcaac atacaaaaaa gtgatgccgc caaaacagaa ataaaccgaa 360

aaccaaaagg gtaaaaactc gaaagtgcca aaaaaaaaac aaataaaaca agaatttcac 420

ttcgaaaaag tgcgtgttct aaaaatatag caacaaatac aaaaccgcaa caaagaagta 480

gcaaatggga ttattttgct gcccaactca acacaaaact gcattttgtt gaattgtata 540

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(57) Abstract: Nucleotide sequences are isolated from Drosophila melanogaster that code for proteins essential for larval viability. These proteins are useful for discovering newinsecticides based on the essentiality of the nucleotide sequences for Drossophila larval viability. Further provided are recombinant proteins and methods for identifying inhibitors to these proteins. Protein inhibitors active in the methods disclosed herein are useful as insecticidal, ectoparasiticidal, antiparasitic, anthementhic and acaracidal agents.